PD - 1/2 101 199 us-09-874-062-2.rge

1. Lano No. 7. 27

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OM nucleic - nucleic search, using sw model

S.C.

June 18, 2003, 05:32:01; Search time 3098 Seconds (without alignments) 10342.863 Million cell updates/sec Run on:

US-09-874-062-2 1101

Title: Perfect score: Sequence:

IDENTITY_NUC Gapox 1.0 Scoring table:

4109280 2054640 seqs, 14551402878 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:*

Database :

1: 9b ba:*
3: 9b_htg:*
3: 9b_htg:*
5: 9b_ov:*
5: 9b_ov:*
6: 9b_ph:*
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em_in:*
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em_ro: em_sts: em_htg_inv:* em_htg_other:* em_htg_pln:* em_htg_rod:* em_htg_mam:* em_htg_mus:'

em_htgo_other:* em_htg_vrt:*

is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	: :	HOMO	HOMO S	Homo sa	Homo sap	Rattus	Rattus	Mus m	AL590997 Mouse DNA	Mus m	Mouse	Homo sa	Нопо	Homo sa	Homo sa	Homo	Mus	Ното	Homo	Homo	Ношо	Ното	HOIIIO	Ношо	Continuation (4 of	Ratt	Mon	Ношо	HOMO S	Homo s	Homo s	Homo s	Homo s	aries	Rattus		Sequence		Sequen	1850	2 Seque	598 Kaposi's	inuation (3 o	06934 Homo sa	snw snw 09	148805 Kaposi'	
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ALIGNMENTS

AC107303

Homo sapiens chromosome 3 clone RP11-595122, WORKING DRAFT SOUTHWELF, 32 unordered pleces.

N AC107303.3 G1:20335965

HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
SM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AC107303 LOCUS DEFINITION

REFERENCE AUTHORS

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Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Boute, J., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Bunke, J., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Bunky, C., Burch, P., Carzon, C., Chavez, D., Chan, G., Chen, R., Chan, Z., Chowdiry, I., Chistopoulos, C., Chen, R., Char, C., Davy, Carroll, L., Dederich, D. A., David, R., David, C., Davy, Carroll, L., Dederich, D. A., David, R., Earnhart, C., Edgar, D., Edward, C., C., Escotto, M., Falls, T., Ferraquto, D., Edward, C., C., Escotto, M., Falls, T., Ferraquto, D., Edward, C., C., Escotto, M., Gorda, J., Garcia, A., Garen, T., Garza, N., Gill, R., Gorsell, J.H., Guevara, W., Gunarathe, P., Hawes, A., Hernandez, J., Harris, C., Horson, R., Jolicet, S., Joudah, S., Karcovic, J., Kelly, S., Khan, W., Holloway, C., Hollins, B., Homai, F., Howard, S., Huber, J., Hulk, S., Youdah, S., Kovar, C., Kratcovic, J., Kureshi, A., Landry, M., Leal, B., Lewis, L.C., Lavis, L., Li, J., Lu, X., Luchtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Mahney, B., McLer, A., Lucier, R., Martin, R., Martin, R., Mahney, E., McLer, M., Mai, G., Metzker, M., Mahney, R., McLer, M., Neador, M., Nordan, M., Yasquez, L., Wera, W., V., Villalon, W., Yason, I., Tanjer, C., Williams, G., Williamson, A., Warce, R., Wanding, S., Walliamson, A., Warce, R., Walling, S., Walliamson, M., Wilcer, W., Y., Willamson, S., Walliamson, M., Wilcer, W., Y., Willamson, S., Walling, S., Nordan, M., Walling, S., Walliams, G., Walling, S., Wa
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Submitted (18-JAN-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 347572)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big bye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 311666 bases at least Q40 Consensus quality: 319305 bases at least Q30 Consensus quality: 344140 bases at least Q20 Estimated insert size: 172965; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc.help@bcm.tmc.edu
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AUTHORS
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JOURNAL
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COMMENT

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
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of 8895 bp in length
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SFRID NO: 2, Lesult & Page Database: GenEmbl; ACNO! ACOOLOTO us-09-874-062-2.rge

05820 TGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTCTAGTTGCTGCAGGCCTTCC 105879 240 480 540 900 721 TGCTGCTGAGGTGAAGCTGCTCTGGATTTGTGCACCTTCTTGCTCTCAACCTTCAGTTCAG 780 781 GCACAGAGTATCTATTCAGAGAACATGTGGACTTCCTGATGTCGTGAAACAGAGGCATG 840 61 GTCTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGAGCTGCTGCCGCCCCAGC 120 121 TGCTGCCAGACCACCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCTGCATTTCCAGT 180 241 TGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGCCTTCC 300 841 GACTGATTTGGAAAATATTTATTAGTATCTATTCTTTTTATAGAAGTTTTTATTGTA 900 301 TGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGC 360 361 TGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGGTGCTGCTAAACCCAGC 420 AGCTGCCCGACCACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCAGTTCT 181 TGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCCTGACCACC 481 TGCTGTATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCAGC 541 TGCTGTATCTCCAGCTGCTACAGGCCCCCAGTGCTGCCAGCCCTGCTGCCGCCCGGGCT 601 TGCTGCATTTCTAGTTGCTGTCATCCCAGCTGCTGTGTGTCCAGCTGCCGCTGCCCTTTC 1 CTGGGAACCCACCCAGCAACCTCCACCCTCTGACGCCATGGTCAGCTCCTGCTGTGGCTCT Gaps Length 347572; 3154 others Indels 13; 2; Score 909.2; DB Pred. No. 6e-148; 0; Mismatches 1 63333 g 108900 t /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3" /clone="RP11-595122" 64859 c 63333 g 10 Ouery Match 82.6%; Best Local Similarity 91.9%; Matches 1002; Conservative 107326 a 661 SASE COUNT Op qq Q g qq qq qq ò g ð qq qq g qq ò ò ò ò ò òγ QQ ò ò 3 ô ò ò

Dipublished

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Baker, J., Baldwin, J., Rarna, N., Beckerly, R., Bann, J., Buthwell, C., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Buthwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cack, P., Corliss, D., Depayre, E., Devon, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Garajery, K., Grant, G., Hagos, B., Healord, A., Herena, L., Horton, L., Howland, J.C., Marquis, N., McEwan, P., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.

Submitted (2b-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Baker J., Baldwin, J., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Calangelo, M., Collins, S., Collymorc, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gagen, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Herena, L., Horlon, L., Howland, J.C., Jones, C., Kann, L., Karutas, A., Lehockky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Mychaleckyj, J., Naylor, J., Naldiff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Kiley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Vo, A., Wagner, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wuyan, D., Ye, W.J. and Zody, M. Direct Submission 106420 GTATCAATT"TCATGTGGAATTGTTTGATGTTCCTCAATAAAACTTCATACTTCATAAAA 106479 106300 TTGAATCTGAATTTACAGTCAAATTCCACATCACATGTTTTAGAACTCTTTTATTTTATT 106359 1021 GTATCAATTTTCATGTGGAATTGTTTGATGTTCCTCAATAAAAGTTCAFACTGTTGAAAA 1080 Homo sapiens chromosome 17, clone hRPK.206_C_20, complete sequence. AC006070 AC006070 AC006070 House Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 961 CAATATACATAAATGTTCAAATGGTATCCTTCTAGATGTTTCTTCCTAATGTTTPCTGTG Submitted (17-DEC-1998) Whitehead Institute/MIT Center for Ge Research, 329 Charles Street, Cambridge, MA 02141, USA On Dec 17, 1998 this sequence vorsion replaced gi:4006456. All repeats were identified using RepeatMasKer: Smit, A.F.A. 1 (bases 1 to 161987) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.206_C_20 106480 GCACCAAAAA 106489 1081 GCAAAAAAA 1090 sapiens. Homo sapiens Unpublished Flormo DEFINITION ORGANISM AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL RESULT 2 AC006070 REFERENCE COMMENT LOCUS ò g ò Db ò g

Only the last 161987 base pairs of this clone are being submitted.

(1996 - 1997)

Green,

TTGAATCTGAATTTACAGTCAAATTCCACATCACATGTTTTTAGAATTCTTTATTCTAATT 960

901

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ACCESSION AC025904 VERSION AC025904 VERSION AC025904 2 G1:7382590 KEYWORDS HTG: HTG: HTGS_PHASE1: HTGS_DRAFT. SOURCE Homo sapiens CRGANISM HOmo sapiens CRANISM HOmo sapiens CRANISM HOmo sapiens FIXATYOLE: Chordata; Craniata; Vertebrata; Entelcostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS BITTEN.B., Linton,L., Nusbaum,C. and Lander,E. TITLE Homo sapieus, clone RP11-585G19 JOURNAL Unpublished REFERENCE 2 (bases I to 174032) AUTHORS BITTEN.B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allcu,N., Anderson,S., Baldwin,J., Barna,N., Bastlen,V., Beda,F.,	Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,	Gradd-Pierre, Grogna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J. C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,	Devine, F. Lieu, C., Luu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M. McEwan, P., McGurk, A. McKernan, K., McPheeters, K., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenqa, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Milanda, C., M	O'MEIL, O'NEATH, O'LIVEL, J. FELESORA, P. FIEFRE, N., Pisani, C., Pollara, V. Raymond, C., Riley, R., Rogov, P., Kuthman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., microcommonder of the common of	TESTAYES, THEOROGE, C., INTESTIAN, TRIGHIU, J., Vassiliev H. (1901), Vo.A., Wilson, W.X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M. TITLE Direct Sutunisation	JOURNAL Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA COMMENT On Apr 1, 2000 this sequence version replaced gi:7249428. All repeats were identified using RepeatMasker:	Smlt, A.F.A. & Green, P. (1990-1997) http://fp.genome.washington.edu/RM/RepeatMasker.html	Center code: wlak Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu	Center project name: 18441 Center clone name: 585_G_19	Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 15871 bases at least 040 Consensus quality: 167389 bases at least 030	Consensus quality: 170660 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 172432; sun-of-contigs Quality coverage: 3.9 in Q20 bases; agarose-fp	Quality coverage: 3.8 in Q20 bases; sum-of-contigs * NOTE: This is a 'working draft' sequence. It currently * consists of 17 contigs. The true order of the pieces	* is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence	* as soon as it is available and the accession number will * be preserved. * 1
Best Local Similarity 94.6%; Pred. No. 2.4e-142; Matches 908; Conservative 0; Mismatches 52; Indels 0; Gaps 0; Qy 131 CCACCTGCAGGACCACCTGCTGCCAGCTGCTGCATTCCAGTTCCTGCAGGC 190 11	Db 138987 AAGGTCTCGCCAGGAGAGCTCCTGCCCAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	Oy 311 CCAGCTGCTGCAAACCCAGCTGCTGCAGCTGCTGCTGCCGCCCAGCTGCTTT 370	Oy 371 CCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGA 430	OY 431 CCACCTGCCGCCCCAGCTGCATTTCTAGTTGCTGCAGGCCTTCCTGTATCT 490 1139227 CCACCTGCTGCCGCCCCAGCTGCATTCTAGTTGCTGCAGGCCTTCCTGTATCT 139286	QY 491 CTAGCTGTTGCAAACCCAGCTGCTGCCACCACCTGCTGCCCCCAGCTGTATCT 550 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 551 CCAGCTGCTACAGGCCCCAGTGCTGCCAGCCTTGCTGCCGCCCGGCTTGCTGCATTT 610 Db 139347 CCAGCTACAGGCCCCAGTGCTGCCAGCCTTGCTGCTGCTGCTGCTGCTTT 139406	Oy 611 CTAGTTGCTGTCATCCCAGCTGTGTGTCCAGCTGCCGCTGCCCTTTCAGCTGCCCGA 670	UY 671 CCACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGGGGGGAGTTCTTGCTGGTGG 730	UY 731 TGAAGCTGCTCTGGATTTGTGCACCTTCTTGCTCTCAACCTTCAGGTACAGAGTA 790	OY 791 TCTATTCAGAGAACATGTGGACTTCCTGATGTCGTGAAACAGAGGCATGGACTGATTTG 850 	Oy 851 GAAAATATTTATAGTATGTATTCTCTTTTATAGAAGTTTTTATTGATCCTATTGAATCTGA 910	Qy 911 ATTTACAGTCAAATTCCACATCACATGTTTTAGAATTCTTTATTCTAATTCAATATACAT 970 Db 139707 ATTTACAGTCAAATTCCAATGTTTTAGAATTCTTTATTCTAATTCAATATACAT 139766	OY 971 AAATCTICAAAIGGIAICCTICTAGAIGTTTCTICCTAATGTITTCTGIGGIAICAATT 1030	Oy 1031 TCATGTGGAATTGTTTGATGTTCCTCAATAAAACTTCATAGTGTTCAAAAGCAAAAAAA 1090 	RESULT 3 AC025904/c LOCUS AC025904 174032 bp DNA linear HTG 26-MAY-2000 DEFINITION Homo sapiens clone RP11-585G19, WORKING DRAFT SEQUENCE, 17

ACU25904 174032 bp DNA linear HTG 26-MAY-2000 Homo sapiens clone RPll-585G19, WORKING DRAFT SEQUENCE, 17 unordered pieces.

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                                                                                                                         bp in length
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                           13204: gap of 100 bp 19430: contig of 6226 bp
                        13105 13204: gap of 100 bp 13105 13206 19430: contig of 6226 bp 19431 19530: gap of 100 bp 19531 25564: gap of 100 bp 25565 5564: gap of 100 bp 31378: contig of 8046 bp 31478 39523: contig of 8046 bp 39524 39623: gap of 100 bp 39524 39623: contig of 7419 bp 39624
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/note="assembly_fragment
clone_end:T7
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/db_xref="taxon:9606"
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Length 174032
                Indels
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Score 735.6; DB 2;
Pred. No. 7.8e-118;
                0; Mismatches
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AJ406935.1 GI:12655443
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 671)
Rogers,M.A., Langbein,L., Winter,H., Ehmann,C., Korn,B. and
                                                                                                                                         Rogers, M.A.

Direct Submission

Submitted (16-OCT-2000) Rogers M.A., Research Program B, German Cancer Research Center, Im Neuenheimer Feld 280, Heldelberg, Germany 69120, GERMANY

Related genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCAGTTCTTGCTGCTGAGTG
                                                                             Characterization of a cluster of human high/ ultrahigh keratin associated proteins on chromosome 17q12 \cdot 21
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/protein_id="CAC27574.1"
/db_xref="G1:12655444"
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/standard_name="KAP4.3"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q12-21"
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Rattus norvegicus clone CH230-115J19, *** SEQUENCING IN PROXRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                               Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases I to 133392)

Worley, K.C.

Direct Submission

Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced gi:17973061.
                                                                                                                                                                                                                                                                                                                                                                                                                      ' NOTE: Estimated insert size may differ from sequence length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.helpebom.tmc.edu
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Center project name: GHAG
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Wurny, D.M., Admans, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabboroks, S. L., Amaretunge, H.C., Are, J.R., Ayele, M., Benks, T., Barboroks, S. L., Amaretunge, H.C., Are, J.R., Ayele, M., Brown, D., Bornin, D., Borbaria, J., Bowley, S., Brieden, M., Brown, E., Brown, M., Bryant, N. P., Balbay, C., Hurch, P., Briede, M., Brown, E., Brown, M., Bryant, N. P., Carron, T.F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, I., Charler, M., Cavazos, S. R., Chacko, J., Chavez, I., Chen, G., Chen, R., Chen, C., Coyle, M.D., Dathorne, S. R., David, K., Dayer, C., Dayer, C., Coyle, M.D., Dathorne, S. R., David, K. J., Delaney, K. R., Draper, H., Dugan-Rocha, S., Durbin, K. J., Barnhart, C., Edgar, D., Edwards, C.C., Elhij, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhij, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhij, C., Escotto, M., Earlhart, G., Edwards, C., Garner, T., Garza, M., Glil, R., Gorell, J. H., Guevae, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Migh, L., Korvah, J., Kovar, C., Kraevot, J., Kureshi, A., Landry, M., Lea, IB., Lewis, L.C., Inwis, L., Li, J., Li, Z., Lichtarge, O., Lieh, C., Liu, J., Liu, M., Luilseyed, H., Meal, M., Mapua, P., Martin, R., Martin, R., Massey, E., Mawhiney, E., Macten, J., Hunk, J., Liu, M., Manu, P., Massey, E., Mawhiney, E., Macten, J., Lui, J., Lui, J., Lui, M., Mayer, A., Moser, M., Nelle, S., Saver, S., Soder, R., Mayer, Sharks, A., Roilbokan, L., Rolfe, M., Manu, Y., Rolfe, M., Nelle, M., Nolden, S., Soder, M., Soder, R., Paren, H., Nelle, M., Nolden, S., Warten, S., Walleren, S., Warten, S., Walleren, S., Walle, M., Yen, W., Yen, Walle, M., Malle, M., Malle, M., Malle, M., Malle, M., Malle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77039, USA on Jul 11, 2002 this sequence version replaced gi:174738%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 143847 bases at least Q40
Consensus quality: 1438653 bases at least Q20
Consensus quality: 153679 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GINS
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Direct Submission
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TITLE
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                                                                           Score 403.4; DB 2; Length 133392;
Pred. No. 3.6e-60;
                                                                                                                                              Indels
             89678: gap of unknown length
91651: contig of 1973 bp in length
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 53 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
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/db_xref="taxon:10090"
/chromosome="11"
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Rummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (Dasea: 1 to 192027).

Betzer, M. L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,

Dederich, D., Thomas, S., Okwucon, G., Carlock, C., Garner, T.,

Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,

Buhay, C., Bunac, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,

Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,

Gorrell, J.H., Gunarature, P., Haller, G., Hernandez, J., Hogues, M.,

Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J.,

Kovar, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Martin, R.,

Massey, E., McLeodd, M.P., Mel, G., Moore, S., Morgan, M., Morris, S.,

Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,

Mulliamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,

Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,

Morris, Lebanission
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On Jan 4, 2001 this sequence version replaced gi:11192108.

Center: Baylor College of Medicine
57190 CATITCIAGCIGCIGCAGGCCIICCIGCIGCGCCCCAGCIGCIGCAITICIAGCIGCIG
                                                                                                                                                                                                                                                                                                                                             666 CCCGACCACCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCGAGTTCTTGCTG
                                                               426 CAGGACCACCTGCTGCCGCCCCAGCTGCTTCTTCTAGTTGCTGCAGGCCTTCCTGCTG
                                                                                   486 TATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCTGCCCCAGCTGCTG
                                                                                                                                                                                                                                   TATCTCCAGCTGCTACAGGCCCCAGTGCTGCCAGCCCTCCTGCTGCCGCCCGGCTTGCTG,
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-------- Project Information
Center project name: MACE
Center clone name: RP23-326H14
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NOTE: This is a working draft's sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
Sequencing vector: M13; L08813
Sequencing vector: M13; L08813; L08813
Chemistry: Dye-primer Bodipy: 57% of reads
Chemistry: Dye-terminator Big Dye: 43% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 191675 bases at least Q40
Consensus quality: 191775 bases at least Q30
Consensus quality: 192401 bases at least Q20
Estimated insert size: 189593; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.8x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TCTGCTCTGACCAGAGCTGTGAAGGTCTGGGCCAGGAGGTGCTGCTGCCGGAAGCT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.4%; Score 378.2; DB 2; Length 192027; 76.7%; Pred. No. 8.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>:</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145312: contig of 28944 bp in length
145412: gap of unknown length
173610: contig of 28198 bp in length
173710: gap of unknown length
190868: contig of 17158 bp in length
190968: gap of unknown length
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71411: gap of unknown length
116268: contig of 44857 bp in length
116368: gap of unknown length
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AL646094 197658 bp DNA linear HTG 27-FEB-2002 Mus musculus chromosome 11 clone RP23-142E7, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                               62 TCTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGAGAGCTGCTGCCGCCCGAGCT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
/note="1327 bases of IS2 transposon (V0061) removed here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                          /notes Sequence from overlapping clone RP23-212C14 (ALS90992). Assembly confirmed by restriction digest." 188825. .188863 /notes Sequence from un1-directional dGTP big dye
                                                                                                                                                                                                                                                                                                                                                                 54968 GCTGCCAGTCTGTGCTGCCAGCCCACCTGCTGCCGCCCCAGCTGCTGCTGCATTTTACAGCT
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HTG: HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                     Length 200602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flanking repeat sequences are irregular.
115074. 115111
                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                Score 378.2; DB 10;
Pred. No. 8.8e-56;
0; Mismatches 143;
                                                                                                                                                       terminator reads only."
40464 c 42904 g 58804 t
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                                                                                                                                                                                                                                                   34.48;
76.78;
                                                                                                                                                                                                                                                                          Best Local Similarity 76.7 Matches 475, Conservative
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEPP: Information on the WORMPEPP.
                                                                                                                                                                                                 34295
                                                                                                                                                         34355
                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse DNA linear ROD 29-NOV-2001 Mouse DNA sequence from clone RP23-132J20 on chromosome 11, AL590997
                                                                                                              541
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-132J20 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (29-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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                                          GCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTTTCTAGTTGCTGCAGGCCTTCCT
                                                                                                              GCTGTATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCAGCT
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∕organism≂"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="11"
/clone="RP23-132J20"
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Blakey, S.
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AL590997/c
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TITLE
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54789

421

54849

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Submitted (29-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeslire, CB10 15A, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On NOV 30, 2001 this sequence version replaced gi:16973v2.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate constitution of the overlapping clone as we seem that an alternate chemistry or covered by high quality data (i.e., phred quality >-
                                                                                                                                                                                                                                                                                                                                      18170 CCGCCCCACTGTTGCATTTCCAGCTGCCGCCCCAGCTGCTGCTGCAGGCCAACTGCTG 18229
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                                                                                                                                                                                                                                                                                                                                                                                                         666 CCCGACCACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCAGTTCTTGTTG 725
                      CAGGACCACCTGCTGCCGCCCCAGCTGCATTTCTAGTTGCTGCAGGCCTTvCCTGCTG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-132420 is from the RPC1-23 Mouse PAC Library constructed by the group of Pieter de Jong.
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This sequence is the entire insert of clone RP23-132320 The true left end of clone RP23-212C14 is at 95441 in this sequence. The true right end of clone RP23-272C1 is at 89011 in this sequence.
                                                                                                                                                                                                              546 TATCTCAGCTGCTACAGGCCCCAGTGCTGCCAGCCCTCCTGCTGCCGCCGGCTTGCTG
                                                                                                                                                                                                                                                                                                             606 CATTTCTAGTTGCTGTCATCCCAGCTGCTGTGTGTCCAGCTGCCGCTGCCCTTTCAGCTG
                                                                                                                486 TATCTCTAGCTGTTGCAAACCCAGCTGCCAGACCACCTGCTGCCGCCCCACTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse DNA sequence from clone RP23-132J20 on chromosome 11, or sequence.
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1 (bases 1 to 200602)
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AL590997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 CAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCCTGACCACCTGCTG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 TATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTG 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                 Direct Submission
Submitted (26-FFB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Feb 28, 2002 this sequence version replaced gi:18135257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 197658; sum-of-contigs
Insert size: 203092; 2.3% error; agarose-fp
Quality coverage: 13.20x in Q20 bases; sum-of-contigs Quality
coverage: 13.17x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. This sequence will be replaced by the finished sequence as soon as it is available the accession number will be preserved.
                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5 Sequencing vector: Alloway Statistics Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 99% of reads Consensus quality: 192802 bases at least 040 Consensus quality: 19297 bases at least 040 Consensus quality: 193039 bases at least 020
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0; Mismatches 178;
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a 42073 c 41216 g 55162 t
                                                                                                                                                               Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
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1. .197658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP23-142E7"
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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Bodyslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Coske, P., DeArcllano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArcllano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArcllano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Gardyna, S., Ginde, S., Goyette, M., Grauch, B.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Klein, J., LaRocque, K., Johnson, R., Jones, C., Kann, L.,
Klein, J., LaRocque, K., Lamazares, R., Macdonald, P., Marquis, N.,
McCartliy, M., McEwan, P., McGurk, A., Macdonald, P., Marquis, N.,
McCartliy, M., McEwan, P., McGurk, A., Macdonald, P., Marquis, N.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oilvar, T., M., Oilver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Killey, R., Rogov, P., Rolman, D.,
Roy, A., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Triqilio, J.,
Vaasiliev, H., Viel, R., Wo, M., Wilson, B., Wu, X., Wyman, D., Ve, W. J.,
Vaasiliev, H., Viel, R., Wo, M., Wilson, B., Wu, X., Wyman, D., Ve, W. J.,
Vassiliev, H., Viel, R., Wo, W., Wilson, B., Wu, X., Wyman, D., Ve, W. J.,
Submitted (16 MAR-2000) Whitehead Institute/MIT Center for Cennome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr. 1, 2000 this sequence version replaced gi:724942H.
All repeats were identified using Repeatbasker:
Sitt, A., Fa, R., & Green, P., 1999-1997)
                                                                                                                                        AC025904 174032 bp DNA Linear HTG 26-MAY-2000
Homo sapiens clone RPI1-585G19, WORKING DRAFT SEQUENCE, 17
                                                                                                                                                                                                                                                                                                                                            Homo sapions
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 174032)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-585G19
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HTG; HTGS_PHASE1; HTGS_DKAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 174032)
                                                                                                                                                                                                 unordered pieces
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
175140 C 175140
                                                                                                                                                                   DEFINITION
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AC025904
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                                                                                                                      Juote=""Yandem repeat. Forced join. Gap size estimated to be approximately 260bp by restriction digest data." 115069, .115073
                                                                                                                                                                                                 115069. 115073
/note="1327 bases of IS2 transposon (V0061) removed here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 TATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCCAGCTGCTG
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                                                                                                                                                                                                                                                                                                                                         (AL590992). Assembly confirmed by restriction digest. 18825. 188863
//octe="Sequence from uni-directional dGTP big dye terminator reads only."
a 40464 c 42904 g 58804 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                           'note="Sequence from overlapping clone RP23-212C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 200602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.4%; Score 368.2; DB 10; Length 72.7%; Pred. No. 4.8e-54; Live 0; Mismatches 178; Indels
                                                                                                                                                                                                                                                           Flanking repeat sequences are irreqular.
115074. .115111
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                                                      /clone="RP23-132J20"
/clone_lib="RPCI-23"
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Best Local S
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66101 74184: contig of 8084 bp in length 74285 gap of 100 bp 74285 86712: contig of 12428 bp in length 86713 86812: gap of 100 bp 86813 103527: contig of 16715 bp in length 103528 102657: contig of 160 bp 103528 120465: contig of 100 bp 120466 12055: gap of 100 bp 120566 145510: contig of 24945 bp in length 120566 145510: contig of 24945 bp in length 120566 145510: contig of 24945 bp in length
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145611 174032: contig of 28422 bp in length.
Location/Qualifiers
                                                                                                                                                                                 8946: yer
13204: gap of 100 bp
19430: contig of 6226 bp in length
19430: contig of 6226 bp in length
100 bp
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66000: contig of 10489 bp in length
                                                                                       2688: gap of 100 bp 645: contig of 3777 bp in length 6565: gap contig of 2281 bp in length
                                                                                                                                                                                                                                                                                                                                                    77: gap of 100 bp 39523: contig of 8046 bp in length 123: gap of 100 bp in length 47042: contig of 7419 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                         42: gap of 100 bp
55411: contig of 8269 bp in length
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74184: contig of 8084 bp in length
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/note="assembly_fragment"
86813. .103527
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103628. .120465
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/note="assembly_fragment"
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/note="assembly_fragment"
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1478. .39523
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5665. .31377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="RP11-585G19"
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                         25664: gap of 10
31377: contig of
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                                                                                                                              6466 6565; gap of

6566 8846; cont.ic

8947 8946; gap of

13105 13204; gap of

13205 13430; cont.ic

13431 9530; gap of

19531 25564; cont.ic

25565 2564; gap of

2564; gap of
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Homo sapieus chromosome 3 clone RP11-595122, WORKING DRAFT SEQUENCE, 32 unordered pieces.
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                                                                                                                                                                       TGCTGCCAGACCACCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTTCCAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 AGCTGCCCGACCACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGGCAGTTCT 720
                                                                                                                                                                                                                     601 TGCTGCATTTCTAGTTGCTGTCATCCCAGCTGCTGTGTCCAGCTGCCGCTGCCTTTTC
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                                                                                                                                                                                                                                                                                                                                                 241 TGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAAAAAATTCC
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                                                                                                                                                                                                          1 CTGGGAACCCACACACACCTCCACCTCTGACGCCATGGTCAGCTCCTGCTGTGCCTCT
                                                                                                                                         Caps
                                                                                                                                       12;
                                                                                                                 Length 174032;
                                                                              1600 others
                                                                                                             32.3%; Score 356; DB 2; Length 17
69.4%; Pred. No. 6.2e-52;
.ive 0; Mismatches 210; Indels
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                                                                              52576
         120566. .145510
/note="assembly_fragment"
145611. .174032
/note="assembly_fragment"
                                           /note-"assembly_fragment
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| 34581 c 34553 g
                                                        clone_end:SP6
                                                                                                                Query Match 32.39
Best Local Similarity 69.49
Matches 504; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.

Edsaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (basea; 1 to 347572)

Alsbrooks; S.L.; Amaratunge, H.C.; Are, J.R.; Ayele, M.; Banks, T.; Barbaria, J.; Bentcon, J.; Binage, K.; Blankenburg, K.; Bonnin, D.; Bouck, J.; Boute, S.; Brieva, M.; Brown, M.; Barks, T.; Barbaria, J.; Burch, P.; Burkett, C.; Burrell; K.L.; Byrd, N.C.; Carrer, M.; Cavazos, S.R.; Chacko, J.; Chavez, D.; Cox, Cox, Cox, L., Cox, Cox, L., Dyrd, N.C.; Cleveland, C.D.; Cox, C.; Cox, L., Dyrd, N.C.; David, R.; Dealandy, K.; Delgado, O.; Denn, A.L.; Ding, Y.; Din, H. H.; Deldandy, C.; Edgar, D.; Edwards, C.C.; Elhaj, C.; Escotto, M.; Falls, T.; Ferraguto, D.; Edwards, C.C.; Elhaj, C.; Escotto, M.; Falls, T.; Ferraguto, D.; Edwards, C.C.; Elhaj, C.; Escotto, M.; Falls, T.; Ferraguto, D.; Edwards, C.C.; Elhaj, C.; Escotto, M.; Falls, T.; Ferraguto, D.; Flagg, M.; Ford, J.; Foster, P.; Frantz, P.; Gorrell, J.H.; Guevara, W.; Guardathe, P.; Halwes, A.; Hannedz, J.; Jacobson, B.; Jai, T.; Johnson, R.; Martin, R.; Martin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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On Apr 28, 2002 this sequence version replaced gi:18449841.
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
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                             HTG; HTGS_PHASE1; HTGS_DRAFT Homo sapiens.
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Unpublished
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                                                                                               Homo sapiens
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                                                                                            ORGANISM
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TITLE
JOURNAL
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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(see http://www.hysc.hcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently
consists of 32 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                       Estimated insert size: 172965; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                    2351: contig of 2351 bp in length 2451: gap of unknown length 6192: contig of 3741 bp in length 6292: gap of unknown length 10339: contig of 4047 bp in length 10439: gap of unknown length
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of 8895 bp in length
         Consensus quality: 331666 bases at least Q40 Consensus quality: 339305 bases at least Q30 Consensus quality: 344140 bases at least Q20
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of 8842 bp in length
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Assembly program: Phrap; version 0.990329
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Pred. No. 6.5e-52;
0; Mismatches 210; Indels
246181: contig of 19753 bp in length
246281: gap of unknown length
265510: contig of 19259 bp in length
295666: contig of 28076 bp in length
293786: gap of unknown length
347572: contig of 53786 bp in length
                                                                                                                                                                 3154 others
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    /organism="Homo sapiens"
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Best Local Similarity
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HSA406936 1099 bp mRNA linear PRI 31-JAN-2001
Homo sapiens mRNA for keratin associated protein 4.4 (KRTAP4.4
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                                                                                                                              Homo sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;

Bammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

(Dases 1 to 1099)

Rogers,M.A., Langbein,L., Winter,H., Ehmann,C., Korn,B. and Schweizer,J.

Characterization of a cluster of human high/ ultrahigh keratin unpublished
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Submitted (16-00T-2000) Rogers M.A., Research Program B, German
Cancer Research Center, Jm Neuenheimer Feld 280, Heidelberg,
Germany 69120, GERMANY
Related genomic sequence: ACO06070 (146419-146919nt)
10.01099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGAGAGCTGCCGCCCCCAGC
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                                                      7.3406936
AJ406936.1 GI:12655445
Keratin associated protein 4.4; KRTAP4.4 gene.
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Pred. No. 7.9e-52;
0; Mismatches 211;
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/db_xref="taxon:9606"
1099 bp
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41. .541
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/clone="sc123"
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Best Local Similarity 69.3%;
Matches 503; Conservative (
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Homo sapiens chromosome 17, clone RP11-619M15, complete sequence. AC037482
                        /product="keratin associated protein 4.7"

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/db_xref="G1:155548.1"

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/translation="MVSSCGSVCSPCTPCCHPSCGSCRPSCCMSSCCRPGCOSOV

VSSCRRPOCCUS
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                                                                                                                                                                   Length 1203;
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                                                                                                                                                                  Score 354.4; DB 9;
Pred. No. 7.9e-52;
0; Mismatches 186;
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/standard_name-"KAP4.7"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                  Characterization of a cluster of human high/ ultrahigh keratin associated proteins on chromosome 17q12-21 Unpublished
                                       TGCTGTATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCAGC
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  TGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGC
                                                                                                                              TGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCATTTCTAGTTGCTGCAGGCCTTCC
                           TGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGC
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Submitted (16-OCT-2000) Rogers M.A., Research Program B, Ger
Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg,
Germany 69120, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Schweizer,J.
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Keratin associated protein 4.7; KRTAP4.7 gene.
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/function="structural protein"
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/db_xref="taxon:9606"
/chromosome="17"
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47. .679
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AJ406939.1
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AUTHORS
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AUTHORS
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JOURNAL
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Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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/organism="Homo sapiens"
/db_xref-"Laxon:9606"
/chromosome-"17"
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/rpt_family~"LIMC5"
complement(1000. .1127)
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/rpt_tamily="L1MA9"
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complement(6526. .6560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2219)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5609, 6042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 619_M_15
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3070. 3031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family-"Alusx"
complement(2682. 294.
/rpt_family-"LIPA8"
2953. 2983
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1154. .1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="LiPA16"
6499, .6580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family-"LTR16C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP!1-619M15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family-"AluSg1"
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4320. .4877
/rpt_family="L1M2b"
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/rpt_family="L1PA5"
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                                                                                                                                                                                                                                      Anderson, S. Baddwin, J. Barna, N. Bastlen, V. Beda, F.,

Boguslavkiy, L. Boukhgalter, B. Brown, A. Burkett, G.

Campoplanon, A. Castle, A. Choegel, Y. Colangelo, M. Collins, S.,

Calmopplano, A. Castle, A. Choegel, Y. Colangelo, M. Collins, S.,

Calmoplano, A. Castle, A. Choegel, Y. Colangelo, M. Collins, S.,

Callymore, A. Castle, A. Choegel, Y. Colangelo, M. Colange, C.

Callymore, A. Castle, A. Choegel, Y. Colangelo, M. Gage, D.,

Galagan, J. Cardyna, S. Cidne, S., Goyette, M. Graham, L. Karatas, M. Kertein, J. Cardyna, S. Cidne, S., Goyette, M. Graham, L. Karatas, M. Kertein, J. Lanceque, Y. Lamazares, R. Landers, T. Lieu, C.

Reding, J. LaRocque, M. Lamazares, R. Landers, T. Uehoczky, J.

Redin, J. LaRocque, M. Lamazares, R. Landers, T. Werherts, R. Medin, J. Meneus, L. Liu, C.

Rocarthy, M. McDean, P. McGurk, A. Wckernan, K. McPheeters, R. Medin, J. Meneus, P. McGurk, A. Wckernan, K. McPheeters, R. Medin, J. Meneus, P. McGurk, A. Wckernan, K. McPheeters, R. Stange-Thomann, M. Stojanov, C. H. Spencer, B.,

Roldin, J. Meneus, L. Liu, G. Theodor, J. McConnor, T. Obonnell, P. Olivar, T. W. Oliver, J. Peterson, R. Petere, M. Pasan, C. Stange-Thomann, M. Stojanov, C. H. Subramanian, A. Talamas, J. Terell, J. Tarvers, M. Trigillo, J.,

Vassillev, H. Wiell, R. Vo, A. Wilson, B. Wu, X. Wyman, D. Ye, M. J.,

Voung, G. Zatinoun, J. Zimmer, A. and Zody, M. Trigillo, J. Wassillev, H. Wield, M. Weller, W. Bastlen, V. Boukhgalter, B. Glasses 1 to 1860/78 | Bastlen, V. Boukhgalter, B. Choegel, Y. Colangelo, M. Collins, S., Collymor, J. Granarder, C. Macdora, A. Kells, C. Maccaro, R. Mark, M. Weller, M. Gage, D., Galagan, J. Granarder, M. McKerran, K. Meldrin, J. Methews, C. McCarthy, M. McKerran, R. Welf, M. Stolanov, C. McGorde, R. Schauer, S. Schuber, S. Schuber, S. Schuber, S. Schuber, J. Hagos, B. W. Wurphy, T. Naylor, M. Weldrin, M. Weldrin, M. Weldrin, M. Weldrin, M. Trigillo, J. Wassiller, H. Welder, M. Riely, R. Rise, C. Rogov, P. Rodore, J. Peterson, W. Peterson, W. Wurphy, T. Naylor, M. Peterson, W. Peterson, 
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Anderson, S., Barnan, N., Babaum, C., Lander, E., Allan, A., Allen, N.,
Anderson, S., Barnan, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand, Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Libey, I., Johnson, R., Johes, C.,
Ferreira, P., Faro, S., Coyette, M., Carala, P., Carala, P., Carala, P., Carala, S.,
Faro, S., Carala, S., Coyette, M., Graham, L., Grand, Pierre, N.,
Faro, S., Faro, S., Coyette, M., Carala, P., Ca
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186078)
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Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McBwan, P., McKernan, K., Meldrim, J., Meneus, L., Mhova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-619M15 Unpublished
ORGANISM
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AUTHORS
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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J. Tophan, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Wol, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-FBB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Feb 23, 2002 this sequence version replaced gi:18693527. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Only the first 186.1 kilobases of this clone are being submitted.
The remainder overlaps accession number AC004231 [WICGR project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smit, A.F.A. & Green, P. (1996-1997)
http://flp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L9334
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comploment(||. 313)
/rpt_family="L1"
complement(314. 642)
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GCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCT
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                                                                                                          GCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCTAGTTGCTGCAGGCTTTCTT
                                                                                                                                                         GCTGTATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCACCT
                                                                                                                                                                                                                                                                                                                         662 GCTGCCCGACCTGCTGTAGAACAACCTGC 693
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Pred. No. 1.2e-51;
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complement (19234. 19392)
/rpt_family="MER4A-int"
complement (19476. 19715)
/rpt_family="MER4A-int"
complement (19864. 20487)
                                                                                                                                                                                                                                          complement 16352. .17004)
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complement (17004. .17056)
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17057. .17295
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complement(17296. .17983)
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18006. .18044
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complement(13700.14460)
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complement(20863, 20961)
/rpt_famil..."
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21759. .21796
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complement(19023, 19224, /rpt_family="LiPA7"
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(8245, .18404
                                                                                                                                         /rpt_family="MER4A-int"
                                           10091, .10547
/rpt_family="L1M2b"
complement(11689, .11981)
/rpt_family="LTR43"
                                                                                           complement(12328, 12677)
/rpt_family="MER4A"
complement(12680, 12776)
/rpt_family="MER4A"
                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(TTTC)n"
complement(18418. .189
 /rpt_family="MIR"
9055. 9346
/rpt_family="Alusc"
10091. .10547
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complement(18046. .
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al Similarity 71.0%;
491; Conservative
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Page

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

protein search, using sw model OM protein Run on:

June 11, 2003, 11:02:46; Search time 18 Seconds (without alignments) 1228.384 Million cell updates/sec

US-09-874-062-3 1484 Title: Perfect score:

1 MVSSCGSVCSDQSCGQGLG......prtccrtrcfHPICCGSSCC 230 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 su

Database :

PIR_73:*
1: pirl:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ultra-high-sulfur	4	σt	hair keratin cyste	cysteine-rich hair	high sulfur protei	high-sulfur kerati	high-sulfur kerati	keratin high-sulfu	high-sulfur wool m	ultra high-sulfur	keratin high-sulfu	high-sulfur wool m	high-sulfur wool m	hypothetical prote	high-sulfur wool m	keratin high-sulfu	high-sulfur wool m	cysteine-rich prot	high-sulfur wool m	high-sulfur wool m			keratin KAP5.5 - s	ultra-high-sulfur	hypothetical prote	keratin high-sulfu	hypothetical prote	hypothetical prote
SUMMARIES	ΙD	A45910	B38346	A38346	S60314	146489	JC6547	S37649	S37650	KRSHHD	I47105	S18946	KRSHHA	147106	147107	T30136	147108	KRSHHC	147111	A55035	147109	147112	KRSHHB	146412	641	99	T29880	KRGT3M	T20561	T18592
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ALIGNMENTS

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RESULT 1

A45910

Litra-high-sulfur keratin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 24-Sep-1999
C;Accession: A45910
C;Accession: A45910
C;Accession: A5910
C;Accession: A65910
C;Accession: A65910
C;Accession: A65910
C;Accession: A65910
C;Accession: A65910
C;Coss-references: CB:M27685; NID:9341749; PIDN:AAA81560.1; PID:91066818
C;Superfamily: ultra-high-sulfur keratin

75; 47.3%; Score 701.5; DB 2; Length 186; 49.0%; Pred. No. 1.1e-42; tive 20; Mismatches 29; Indels 75 Best Local Similarity 49.0 Matches 119; Conservative Query Match

58 SCCKPSCCLITICGRITICGRPSCCISSCCRPSCCISSCCRPSCCRITICGRPSGCISSCCRP 117 118 SCCISSCCKPSCCHTTCCKPSCCISSCCKPSCCISSCCKPSCCQTTCCKPSCCISSCYRP 177 87 1 MVSSCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSC---CISSCCRPSCCIS 57 46 ò g ò g ò

178 QCCQPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCCRTTCFHPIC------CGS 227 qq ò

q

111 SCC 181 179 ογ qq

RESULT 2

ultra-high-sulfur keratin 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; H38346
R;Wood, L.; Mills, M.; Halzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 266, 40'44, 1991
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and ski A;Reference number: A38660; MUID:194154184; PMID:1840598

us-09-874-062-3.rpr

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cysteine-rich hair keratin associated protein - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_chauge 24-Scp-1999 C;Accession: 146489; S49201 Nesci, A. Differentiation 58, 227-232, 1995 A;Teferentiation 58, 227-232, 1995 A;Teference number: 146489; MulD:95228955; PMID:7536172
                                                                                                  hair keratin cysteine rich protein - sheep
(Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(Spate: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 24-Scp-1999
(SAccession: S60314
R.Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.
J. Invest. Dermatol. 102, 178-185, 1994
A; Title: Dietary cysteine requiates the levels of mRNAs encoding a lamily of cysteine
A; Reference number: S60314; MUID:94189288; PMID:7508963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCC 120
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     179 QSSCCKPCCQSSCCKPCCQSSCCKPCCQSSCCKP-CCSS-----GCGSS/CQDSC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVSSCGGSVCSDQSCGQCLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVSSCCGSVCSAQSCGRSLCQETCCRPSCCQTTCCRTTCYRPSCGVSSCCRP------
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                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-151 cFRA-
A;Cross-references: EMBL:X73462; NID:9512030; PIDN:CAA51841.1; PID:9512031
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-126 <PCM>
A;Cross-references: EMBL:X80035; NID:9510540; PIDN:CAA56339.1; PID:4510541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.7%; Score 619; DB 2;
61.6%; Pred. No. 5.7e-37;
ive 13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.4%; Score 569.5; DB 2 Best Local Similarity 57.7%; Pred. No. 1.5e-33; Matches 90; Conservative 15; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 61.69
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-126 <POW>
                                                                                                                                                                                                                                                                                                                                        A; Accession: S60314
A; Status: preliminary
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     g
                                                                        A.Cross-references: GB:M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964
A.Note: this is a correction
R.Note: this is a correction
R.Nood, L.: Mills, M.: Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A:Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin (A:Reference number: A38346; MUID:91065960; PMID:2250030
A:Accession: B38346
A:Molecule type: DNA
A:Residues: 1-21, GGCGSGCGGGGCSCCKPVCC', 22-40, GSS', 44-45, 'G', 47-48, 'S', 50, 'GSS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Mus musculus (house mouse)
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
C:Accession: A38346
K:Mood, L.; Mills; M.; Hatzenbuhler, N.; Vogeli, G.
V.; Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and A;Reference number: A38346; MUID:91065960; PMID:2250030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSC--CGSVCSDQSCGQGLG-----QESCCRPSCCQTTCCRTTCCRPSCCISSC-- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSCGGGSSCG--GCGSGCGGCGSNCGGCGSSCCKPVCC---CKPVCCCVPVCSCSSCGG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SCCGSVCS---DQSCGQGLGQESCCRPSCC-----QTTC--CRTTC----CRPSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TCCG--CSGGCGSSCG-GCG-SSCCKPVCCCVPVCSCSSCGGCKGCCGSCGGCKGGCGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSC
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                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GB:M37759; NID:9200961; PIDN:AAA40106.1; PID:9200962
A:Note: the sequence reported in this paper has been corrected. See A38660
C:Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-230 <WOO>
A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 693.5; DB 2;
52.7%; Pred. No. 4.4e-42;
tive 23; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ultra-high-sulfur keratin 1 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 52.7% ies 119; Conservative
A;Accession: A38660
A;Molecule type: DNA
A;Residues: 1-223 <WO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C; Accession: S37650
C; Accession: S37650
Mol. Biol. 26, 550-555, 1992
A; Title: Cloning and Structural characterization of human hair sulfur-rich keratin ge A; Accession: S37650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Powell, B.C.; Sleigh, M.J.; Ward, K.A.; Kogers, G.E.
Nucleic Acids Res. 11, 5327-5346, 1983
A;Title: Mammalian keratin gene families: organisation of genes coding for the A;Reference number: S07349; MUID:83299218; PMID:6193483
A;Accession: S07911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: keratin high-sulfur matrix protein IIIA
C;Keywords: duplication; halr
F;2-182/Product: keratin high-sulfur matrix protein B2D #status predicted <MAT>
F;27-36,37-46,47-56,57-66,67-76,77-86/Region: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --CKFFC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ACCQTSFCGFPSCSTSGTCGSSCCQPSCCETSSCQPRCCETSCCQPSCCQTSFCGFFSFS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <2HU>
A;Cross-references: EMBL:X63337; NID:g311879; PIDN:CAA44937.1; PID:q311880
C;Superfamily: keratin high-sulfur matrix protein IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 SCCQTTCCRTTCCRPS-CCISSCCRPSCCISSCCKPSCCLTTCCRTTCCRPSCC-ISSCC
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A;Residues: 1-182 <POW>
A;Cross-references: EMBL:X01610; NID:g1295; PIDN:CAA25759.1; PID:g1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 177;
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44.0%; Pred No 3e-25;
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                                                                                                                                                                      high-sulfur keratin - human
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Best Local Similarity
Matches 80; Conserv
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192 SSCCH 196
                                          170 YSCSH 174
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TC 177
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Best Local Simi
Matches 76;
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high-sulfur keratin - human
C;Species: Homo sapiens (man)
C;Dacies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: 537649
R;Zhumabaewa B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A;Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A;Reference number: 537649
A;Status: preliminary
                                     C;Species: Rattus norregicus (Norway rat)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Dates: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
R;Astille; S; Obuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A;Title: Structure and hair follicle-specific expression of genes encoding the rat high A;Reference number: JC6547; MUID:98201605; PMID:9524245
A;Reference number: JC6547
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                A;Residues: 1-188 <MIT>
A;Cross-references: DDBJ:AB003753; NID:g3046870; PIDN:BAA25573.1; PID:g3046871
C;Comment: This protein is a cysteine-rich, keratin associated protein.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCC------RTTC- 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-175 <ZHU>
A;Cross-references: EMBL:X63338; NID:g311881; PIDN:CAA44938.1; PID:g311882
C;Superfamily: keratin high-sulfur matrix protein IIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Indels
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C;Superiamily: keratin high-sulfur matrix protein IIIA
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Pred. No. 8.1e-33;
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47.2%; Pred. No. o.-
''e 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Conservative
                      high sulfur protein B2E - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                          A; Cross-references:
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Best Local Similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.Alternate names: UHS keratin; ultra high-sulfur matrix protein C.Species: Homo sapiens (man)
C.Accession: S18946; B3686
R.Drabent, B.; Doenecke, D.
Submitted to the EMBL Data Library, December 1991
A.Description: Nucleotide sequence of a Human high-sulphur keratin cDNA.
A.Reference number: S18946
A.Molecule type: mRNA
A.Residues: 1.169 CDRA
A.Molecule type: mRNA
A.Cross references: EMBL:X63755; NID:932471; PIDN:CAA45283.1; PID:932472
R.MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Call Biol. 111, 2587-2600, 1990
A.Title: Structure and expression of genes for a class of cysteine-rich proteins A.Recession: B36686; MUID:91115951; PMID:1703541
A.Accession: B36686
A.Molecule type: DNA
A.Residues: 1-39, 'Y', 41-169 <AACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCCISSCCR-PSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TSCCQPTSIQTSCCQPTCLQTSGCETGCGIGGSIGYGQVGSSGAVSSRTRWCRPDCRVEG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCRPSCCISSCCKPSCC----QTTCCRPSCCISSCYRPQ-CCQPSCCRPACCISSCCHP 197
----TSIQTSCCQPISIQTSCCQPTCLQTSGCETGCGIGGSIGYGQVGSSGAVSSRTKW 112
                                           CRPSCCISSCCRPSCCISSCCKPSCC----RTTCCRPSCCISSCCRPSCCISSCCKPSC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High-sulfur wool matrix protein B2A - sheep
CiSpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
CiSpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
CiSpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
CiAccession: 147105
Rikogers, G. R.; Hickford, J.G.; Bickerstaffe, R.
Anim. Genet. 25, 407-415, 1994
Anim. Genet. 25, 407-415, 1994
A.Title: Polymorphism in two genes for B2 high sulfur proteins of wool.
A:Reference number: 147105
A:Reference number: 147105
A:Accession: 147105
A:Residues: 1182 * ReGS
A:Residues: 1182 * ReGS
C:Superfamily: keratin high-sulfur matrix protein 111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.1%; Score 432; DB 2; Length 18
40.7%; Pred. No. 6.5e-24;
Live 25; Mismatches 57; Indels
                                                                                                                                                            COTTCCRPSCISSCYRPQCCQPSC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ultra high-sulfur keratin 1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 40.7
Matches 74; Conservative
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TC 182
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A. Molecule type: protein
A. Residues: 2-172 < FLL>
A. Residues: 2-172 < FLL>
A. Residues: 2-172 < FLL>
A. Note: a minor component has 13-Thr, 23-Asn, and 24-Phe
C. Comment: The keratin products of mammalian epidermal derivatives such as wool and h
fur and high-tyrosine keratins, having molecular weights of 6-20 kilodaltons, whereas
C. Superfamily: keratin high-sulfur matrix protein IIIA
C. Keywords: acetylated amino end: blocked amino end: duplication; hair
F: 2-172/Product: keratin high-sulfur matrix protein B2A #status experimental <MAT>
F: 27-76/Region: 10-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RyPowell, B.C.; Sleigh, M.J.; Ward, K.A.; Rogers, G.E.
Nucleic Acids Res. 11, 5327-5346, 1983
A;Title: Mammalian keratin gene families: organisation of genes cuding for the B2 hig A;Reference number: S07349; MUID:83299218; PMID:6193483
A;Accession: S07910
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A;Cross-references: EMBL:X01610; NID:g1295; PIDN:CAA25757.1; PID:g1296
A;Cross-references: EMBL:X01610; NID:g1295; PIDN:CAA25757.1; PID:g1296
Biochem. J. 130, 833-845, 1972
Biochem. J. 130, 833-845, 1972
A;Title: The amino acid sequence of protein SCMK-B2A from the high-suiphur fraction A;Reference number: A02837; MJID:73224964; PMID:4679226
A;Reference number: A02837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 SCSSCGRRGCGSCGSSCGSCGSGCGSSCCQSSCCQCSCCCRVYCSQCSC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keratin high-sulfur matrix protein B2A - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 24-Apr.1984 #sequence_revision 12-Apr.1996 #text_change 22-Jun-1999
C;Accession: S07910; A02837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SGGCGSSCGGCDSSCG------SCGSGCRGCGPSCCAPVC----CCVPAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SSCCGSVCS--DQSCCQGLCQESC-----CRPSCCQTTCCRTTCCRPSCC1SSCCRPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 CKP-CCSSSGRGSSCCQSSCCKP-CCSSGCGSSCCKPCCSQSRCCVPVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 CRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCKPSC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 431.5; DB 1;
Pred. No. 6.8e-24;
                   A,Map position: 11913-11913
C;Superfamily: ultra-high-sulfur keratin
C;Keywords: hair: tandam repeat
E;7-15Kegion: Ser-rich nonapeptide repeat
F;69-18Kegion: Gly-rich decapeptide repeat
F;69-18Kegion: Gly-rich decapeptide repeat
F;79-88Kegion: Gly-rich decapeptide repeat
F;79-18Kegion: Cys-rich decapeptide repeat
F;79-10/Region: Cys-rich decapeptide repeat
F;189-10/Region: Cys-rich decapeptide repeat
F;181-11/Region: Cys-rich decapeptide repeat
F;187-18/Region: Cys-rich decapeptide repeat
F;117-18/Region: Ser-rich nonapeptide repeat
F;187-18/Region: Cys-rich decapeptide repeat
F;187-18/Region: Cys-rich decapeptide repeat
F;186-15/Region: Cys-rich decapeptide repeat
F;186-15/Region: Cys-rich decapeptide repeat
F;186-15/Region: Cys-rich decapeptide repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
GDB:125257; OMIM:148021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.18;
46.98;
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Best Local Similarity 37.6%
Matches 76; Conservalive
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Qy 87 PSCCISSCCKPSC	RESULT 15 T30136 hypothetical protein C14C11.8 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct 1999 #sequence_revision 15-Oct 1999 #text_ C; Accession: T30136 R; Du, Z.; Gattung, S. Submitted to the EMBL Data Library, March 1996 A; Description: The sequence of C. elegans cosmid C14C11. A; Reference number: 220742 A; Accession: T30136 A; Accession: T30136 A; Accession: T30136 A; Regidues: 1-654 < DUX. A; Regidues: 1-654 < DUX. A; Regidues: 1-654 < DUX. A; Experimental Source: EMBL: U53141; PIDN: AAA96110.1; GSPDB: C; Genetics:	A, Genes: CLESP:CLAGII: 8 A, Map position: 5 A; Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; Query Match Best Local Similarity 26.4%; Pred: No. 1.1e-19; Matches 114; Conservative 33; Mismatches 73; In	Qy 3 SSC-CGSVCSDQSCG	252 IVVQQPQQQQ 80CISSCCR 1: 1 312 QPSCVQAACA 120 372 QPKCSSQCVE	144 431 431	Db 487 QSACQPSCQSNTQCVQAC-IP-SCQQTCGQQAQPVIVVQ Qy 218 TCFHPICCGSSC 229
63 SCCLTTCCRTTCCRPSCCISSC	RESULT 13 147106 high-sulfur wool matrix protein B2A - sheep high-sulfur wool matrix protein B2A - sheep c.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C.Spaces: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 15-Sep-2000 C.Spaces: 3.0n: Hickford, J.G.; Bickerstaffe, R. R. Rogers, G. R.; Hickford, J.G.; Bickerstaffe, R. Anim. Genet. 25, 407-415, 1994 A.Title: Polymorphism in two genes for B2 high sulfur proteins of wool. A. Reference number: 147105; MUID:95209146; PMID:7695121 A. Accession: 147106 A. Status: preliminary; translated from GB/EMBL/DDBJ A. Residues: 1-172 < RGG> A. Residues: 1-172 < RGG> C. Superfamily: keratin high-sulfur matrix protein JIIA	Ouery Match Best Local Similarity 42.5%; Pred. No. 7.76-22; Matches 74; Conservative 21; Mismatches 59; Indels 20; Gaps 6; 43 SCCISSCCR-PSCCISSCCRPSCCLTTCRTTCRPSCCISSCCRPSCR 101 1 11 1 1 1 1 1 1 1 1		HESULT 14 147107 high-sulfur wool matrix protein B2A - sheep C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C; Species: 1997 #sequence_revision 21-Feb-1997 #text_change 15-Sep-2000 C; Accession: 147107 R; Rogers, G.R.; Hickford, J.G.; Bickerstaffe, R. Anim. Genet. 25, 407-415, 1994 Arithe: Polymorphism in two genes for B2 high sulfur proteins of wool.	A: Accession: 147107 A: Accession: 147107 A: Status: preliminary; translated from GB/EMBL/DDBJ A: Molecule type: DNA A: Molecule type: DNA A: Residues: 1-162 <rgg> A: Cross-reterences: GB:L33887; NID:q499873; PIDN:AAB01446.1; PID:g940357 C: Superfamily: keratin high-sulfur matrix protein IIIA</rgg>	Query Match 25.9%; Score 384.5; DB 2; Length 162; Best Local Similarity 37.1%; Pred; No. 1.2e-20; Matches 69; Conservative 20; Mismatches 48; Indels 49; Gaps 6; 28 SCCQTTCCR-TTCCRPSCCISSCCRPSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCR 86 11 </td

dels 212; Gaps 29; RPSCCISSCYRPG/CQPS 183 3N00023; CESP:C14C11.8 SC---CISSC------ 59 :1 | | | | | | | SCQPMCSSSCVUQQQQ1 251 (: L LTI ZQNQQQNQCTSSCMPSC 311 -----CRT 217 1: DOPOGNICVOACUPOCOO 544 CRPSCCOTTC---- 34 522/3; 543/3; 586/3 -----7TFCCRPSC 79 _change 15-0xt-1999 th 654;

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Sequence 2, Appli
Sequence 10890, A
Sequence 25, App
Sequence 14, Appl
Sequence 27528, A
Sequence 23764, A
Sequence 1390, Ap
Sequence 1390, Ap
Sequence 5295, Ap
Sequence 5295, Ap
Sequence 2070, Ap
Sequence 377, Appli
Sequence 2070, A
Sequence 375, Ap
                                                                                                                 June 18, 2003, 15:10:00 ; Search time 224 Seconds (without alignments) 7212.667 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-864-761-10890
US-09-962-832-225
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                                                                                                                                                                                                                                                                                                                                                  1042519 segs, 733713590 residues
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                                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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20 114.4 10.4 573 10 21 112.6 10.2 22885 9 23 110.2 10.1 1862 10 23 110.5 6 9.6 2313 9 25 105.6 9.6 2313 10 25 105.6 9.6 2313 10 26 25 105.6 9.6 2313 10 27 10.3 9.4 1967 10 28 102.2 9.3 3015 9 31 99.8 9.4 1967 9 28 30 100.2 9.1 3331 9 31 99.8 9.6 9.0 1449 9 28 31 99.8 9.0 1449 9 29 9.0 1822 9 39 96.6 9.0 1822 9 30 90.6 8.7 657 10 44 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 45 92.4 8.4 1008 10 46 92.4 8.4 1008 10 47 8PLIOR APPLICATION NUMBER: 60/7 PRIOR PILING DATE: 1999-12-01 NUMBER OF SEQ 1D NOS: 3 SOFTWARE: PATENTING DATE: 1999-12-01 NUMBER OF SEQ 1D NOS: 3 SOFTWARE: PATENTING DATE: 1999-12-01 TYPE: DAA ORGANISM: HOMO SAPIENS A CTGGGAACCCACCACACACACACACACACACACACACACA	US-09-864-761-5592 US-09-764-891-6987 US-09-669-852-4 US-10-017-270-510 US-09-68-4-13-157 US-09-78-973-157 US-09-78-973-157 US-09-864-761-5097 US-09-864-761-5097 US-09-864-761-5097 US-09-864-761-5097 US-09-964-373-658-31 US-09-962-832-225 US-09-973-965-1601 US-09-954-456-1601 US-09-954-469-3 US-09-922-469-3 US-09-922-469-3 US-09-922-469-1	ALIGNMENTS 14062 Ifide Core Domain-Contaides, and Antibodies 5/09/874,062 06 1050/32462 168,229	Score 1101; DB 10; Pred. No. 2.8e-260; 0; Mismatches
20 114.4 21 112.6 22 110.1 23 110.1 23 110.1 24 105.6 25 105.6 26 27 105.6 27 105.6 28 100.2 28 100.2 29 100.2 29 100.2 29 100.2 31 99.8 20 33 98.6 23 34 98.6 23 36 98.6 23 36 98.6 23 37 99.6 24 10 99.8 25 90.4 44 92.4 44 92.4 44 92.4 44 92.4 44 92.4 44 92.4 44 92.4 44 92.4 44 92.4 44 92.4 45 92.4 47 92.4 48 92.4 48 92.4 49 92.4 41 92.4 42 92.4 44 92.4 45 92.4 47 92.4 48 92.4 48 92.4 49 92.4 41 92.4 41 92.4 42 92.4 44 92.4 45 92.4 44 92.4 45 92.4 44 92.4 45 92.4 47 92.4 48 92.4 48 92.4 48 92.4 49 92.4 49 92.4 40	22885 9 22885 9 10 1882 9 10 1882 9 10 1882 9 10 1882 9 11 1882 9 12 18 18 18 13 18 18 18 14 18 18 18 18 16 18 18 18 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	pplication US/0987 20020081607A1 MATTON: Uben et al. Uben et al. EMITON: Four Disul EMITON: Pour Disul CE: PT033P1 ICATION NUMBER: US MC DATE: 2001-129 DATE: 2000-11-29 DATE: 1999-12-01 Q ID NOS: 3 tentin Ver. 2.0	mlarity 100.0% Conservative TGGGAACCCACGAA TGGGAACCCACCAGAG TTTTCTTTTTTTTTT
	01784597860178459786017845	RESULT 1 US-09-874-062-2 Sequence 2, Agreence 2, Agreence 1, Agreence 2, Agreence 2, Agreence 2, Agreence 2, Agreence 2, Agreen 2, Agreence 2, Agreenc	Match Local S local S local S li01 les li

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D IN LUNG, SIGNAL - 1.4
D IN BRAIN, SIGNAL - 1
D IN BONE MARROW, SIGNAL - 1.1
D IN FEFAL LIVER, SIGNAL - 1.3
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FILE KEFEKELE: ACGINICA'A' DE CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR PILLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR PELLING DATE: 2000-010-04
PRIOR PELLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2000-06-30

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Pred. No. 8
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Best Local Similarity 71.2%;
Matches 306; Conservative
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Patent No. US20020048763A1
GENERAL INFORMATION:
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TITLE OF INVENTION:
GENE EXPRESSION ANALYSIS BY MICROARRAY
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TCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGAGAGCTGCTGCCGCCCCAGCTGCTGC 126
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                CCTGCTGCCGCCCCAGCTGCTGTATCTCCAGCTGCTACAGGCCCCCAGTGCTGCCAGCCCT
                                  Length 8705;
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APPLICANT: Ruffner, Duane E.
APPLICANT: Pierce, Michael L.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zhidong
FILE REFERENCE: T6678.US.A
CURRENT APPLICATION UNMARE: US/10/291,230
CURRENT APPLICATION UNMARE: US/0/291,230
PRIOR APPLICATION NUMBER: US 99/647,344
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1998-03-28
PRIOR FILING DATE: 1998-03-28
PRIOR FILING DATE: 1998-03-28
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Version 3.1
SEQ ID NO 14
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Pred. No. 1.9e-30;
); Mismatches 336;
                                                                                                                                                                                                                        Sequence 14, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
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ilarity 53.0%;
Conservative
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Best Local Similarity
Matches 382; Conserv
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APPLICANT: Enner, Reinhard
APPLICANT: Enner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
SEQ ID NO 225
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                                                                                                             GCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGCT 421
GCTCTCAGACTACCTGCTGCCAGACCACTTGCTGTCGCCCCAGCTGCTGCTGCCACCCAGTCT 280
                                                                                             GCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCT
                               GCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTTCCAGTTGCTGCAGGCCTTCCT
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|GCTGTCAGAC 461
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; ORGANISM: Homo sapiens
US-09-962-832-225
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David K.
APPLICANT: Harzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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N: EXPRESSED IN LUNG, SIGNAL = 1.4
N: EXPRESSED IN BRAIN, SIGNAL = 1.1
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
N: SWISSPOT HIT: 075690, EVALUE 6.00e-10
N: STILUDANN HIT: BE290684.1, EVALUE 3.00e-11
N: NT HIT: X73462.1, EVALUE 6.00e-15
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Pred. No. 8.9e-31;
0; Mismatches 126;
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEO ID NGS: 49117
SOFTWARE: Annomax Sequence Listing Engine v
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Patent No. US20020048763A1
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Best Local Similarity 67.5%;
Matches 280; Conservative (
                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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OTHER INFORMATION: MOTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
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US-09-864-761-6314/c
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APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                      427 AGGACCACCTGCTGCCGCCCCAGCTGCATTTCTAGTTGCTGCAGGCCTTCCTGCTGT
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PLILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-05-06
PRIOR PLILING DATE: 2000-06-05-06
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-07
PRIOR PLILING DATE: 2000-09-07
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00667
PRIOR PAPLICATION NUMBER: PCT/USO1/00667
PRIOR PAPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PPLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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PRIOR PPLING DATE: 2001-01-30
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PRIOR PPLING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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US-09-864-761-27528
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/235,366
PRIOR PILING DATE: 2000-09-03
PRIOR PELING DATE: 2000-01-00-04
PRIOR PILING DATE: 2000-01-00-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 2001-01-30
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PRIOR PELING DATE: 2001-01-30
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DR APPLICATION NUMBER: PCT/US01/00661
DR APPLICATION NUMBER: PCT/US01/00670
DR FILING DATE: 2001-01-30
DR FILING DATE: 2001-01-30
DR APPLICATION NUMBER: US 60/234,687
DR FILING DATE: 2000-09-21
DR FILING DATE: 2000-09-21
DR FILING DATE: 2000-06-30
DR FILING DATE: 2000-06-30
DR FILING DATE: 2000-06-30
DR APPLICATION NUMBER: US 09/774,203
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Patent No. US20020048763A1
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN DACENTA, SIGNAL = 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00069

OR APPLICATION NUMBER: PCT/US01/00669

OR FILING DATE: 2001-01-30

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00668

OR APPLICATION NUMBER: PCT/US01/00668

OR APPLICATION NUMBER: PCT/US01/00669

OR APPLICATION NUMBER: PCT/US01/00660

OR APPLICATION NUMBER: PCT/US01/00600

OR APPLICATION NUMBER: PCT/US01/00600

OR APPLICATION NUMBER: PCT/US01/00600

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                NR APPLICATION NUMBER: US 60/236,359
NR FILING DATE: 2000-10-04
NR FILING DATE: 2000-09-27
NR FILING DATE: 2001-01-30
NR APPLICATION NUMBER: PCT/US01/00667
NR APPLICATION NUMBER: PCT/US01/00667
                                                                                   PRIOR APPLICATION NUMBER: US 00/180, 112
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-07
PRIOR PLILING DATE: 2000-10-130
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
APPLICATION NUMBER: US/09/864,761
FILING DATE: 2001-05-23
                             CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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Best Local Similarity 64.2
Matches 319; Conservative
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ORGANISM: Homo sapiens
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US-09-864-761-6314
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE PEFERENCE: Acomica-X-1
                                                                                                                       601 TGCTGCATTTCTAGTTGCTGTCATCCCAGCTGCTGTGTGTCCAGCTGCCGCTGCCCTTTTC 660
TGCTGCAGGACCACCTGCTGCCGCCCCCAGCTGCATTTCTAGTTGCTGCAGCCTTCC 480
                      TGCTGTATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCGCCCAGC 540
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N: EXPRESSED IN PLACENTA, SIGNAL = 2.4

N: EXPRESSED IN BRAIN, SIGNAL = 2.5

N: EXPRESSED IN BRAIN, SIGNAL = 2.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

N: EXPRESSED IN LUVG, SIGNAL = 2.5

N: EXPRESSED IN LUVG, SIGNAL = 2.5

N: EXPRESSED IN HELA, SIGNAL = 2.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4

N: EXT_HOMAN HIT: BE250684.1, EVALUE 4.00e-07

N: MIT: 917657286, EVALUE 8.00e-20

N: SWISSPROT HIT: P02438, EVALUE 7.50e-02
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Publication No. US20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEO ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 146.6; DB 10; Length
65.0%; Pred. No. 3.2e-26;
ive 0; Mismatches 134; Indels
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22764
LENGTH: 403
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; ORGANISM: Homo sapiens
US-10-092-154-1390
                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                  OTHER INFORMATION: E. OTHER INFORMATION: E.
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OTHER INFORMATION:
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US-09-864-761-22764
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US-10-092-154-1390
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                                                                                       222 CAGCTGCTGACCGCTGCTGCTGCAGGACCACGTGCTGCCGCCCCCAGCTGCTGCTATTTC
                                                                                                                                5348 CAGAAGCCCACCCTCCATCCCTGACACCATGACCCACTGTTGCTCCCCTTGCTGTTGAGCC
                                                                                                                                                                            282 CAGTIGCIGCAGGCCTICCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTTGTAGGAC
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Length 11872;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009, Nucleic Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEO ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
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                                           Indels
Score 142; DB 9; L. Pred. No. 4.1e-24; 0; Mismatches 185;
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60.8%; Pred. No. 4.1e-24;
live 0; Mismatches 185;
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  12.9%;
60.8%;
Query Match 12.9°
Best Local Similarity 60.8°
Matches 305; Conservative
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US-09-764-847-1390
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Matches 3(
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Sequence 4747, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACT! PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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WEXPRESSED IN LENRY, SIGNAL = 1.9
WEXPRESSED IN LUNG, SIGNAL = 1.9
WEXPRESSED IN HELA, SIGNAL = 1.9
WEXPRESSED IN FETAL LIVER, SIGNAL = 1.6
WEXPRESSED IN BRAIN, SIGNAL = 1.9
WEXPRESSED IN BONE MARROW, SIGNAL = 1.8
WEXPRESSED IN ADULT LIVER, SIGNAL = 1.8
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ilarity .64.0%; Pred. No. 6.5e-24;
Conservative 0; Mismatches 136;
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION UNMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine ver
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ORGANISM: HOMO
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Tenn, Sharron G.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aconica-X.
FILE REFERENCE: Aconica-X.
CURRENT PALLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/203,366
PRIOR APPLICATION NUMBER: US 60/203,366
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PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-130
PRIOR FILING DATE: 2001-130
PRIOR PLING DATE: 2001-130
PRIOR APPLICATION NUMBER: PCT/US01/0066
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FREERL INFORMATION:

APPLICANT: FRUIN, SHATFOU C.

APPLICANT: How, SHATFOU C.

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FILLE OF INVENTION: HOWEN CENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOURTH APPLICANTON NUMBER: US/09/04/761

CURRENT APPLICANTON NUMBER: US/09/04/761

CURRENT APPLICANTON NUMBER: US/09/06/32/36

PRIOR PELLING DATE: 2001-05-23

PRIOR FILLING DATE: 2000-05-27

PRIOR PELLICATION NUMBER: US/09/36/36/36

PRIOR PELLICATION NUMBER: US/09/36/36/36

PRIOR PELLICATION NUMBER: US/09/36/36/36

PRIOR PELLICATION NUMBER: PCT/US/01/06/66

PRIOR PELLICATION NUMBER: PCT/US/01/06/66

PRIOR PELLICATION NUMBER: PCT/US/01/06/67

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PRIOR PELLICATION NUMBER: PCT/US/01/00/66

PRIOR PELLICATION NUMBER: PCT/US/01/06/69

PRIOR PELLICATION NUMBER: PCT
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Patent No. US20020048763A1
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N. EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

N. EXPRESSED IN ADULT LIVER, SIGNAL = 1.3

N. EXPRESSED IN BONE MARROW, SIGNAL = 1.3

N. EXPRESSED IN LUNG, SIGNAL = 1.5

N. EXPRESSED IN PLACENTA, SIGNAL = 2

N. EXPRESSED IN HELIOO, SIGNAL - 1.3

N. EXPRESSED IN HELIOO, SIGNAL - 1.3

N. EXPRESSED IN HELA, SIGNAL - 1.3

N. EXPRESSED IN HELA, SIGNAL - 1.5

N. EXPRESSED IN HERAT, SIGNAL - 1.5
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4747
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llarity 51.8%; Pred. No. 2.7e-23;
Conservative 0; Mismatches 289;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLLING DATE: 2000-08-26
PRIOR PLLING DATE: 2000-08-26
PRIOR PAPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR PLLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR PLLING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: EX-
OTHER INFORMATION: EX-
OTHER INFORMATION: EX-
OTHER INFORMATION: E-
OTHER INFORMATION:
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ses 310; Conserv
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OTHER INFORMATION:
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Matches
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; ORGANISM: Homo sapiens
US-09-874-062-2
                                                              Query Match
Best Local Similarity
Matches 318; Conserv
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APPLICANT: Ruben et al.
TITLE OF INVENTION: POLYPETIGE Core Domain-Containing (FDCD) Polynucleotides,
TITLE OF INVENTION: Polypeptides, and Antibodies
FILE REFERENCE: PT033P1
CURRENT APPLICATION NUMBER: US(0)/874,062
PRIOR APPLICATION NUMBER: DCT/US00/32462
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEO ID NOS: 3
SOFTWARE PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                      101 AGAGCTGCTGCCGCCCCAGCTGCTGCCAGACCACCTGCTGCAGGACCACCTGCTGCCGCC 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACCTGTGTGA---CCAGCTGCTGCCAGCCTTCCTGCTGCAGCACACCCTGCTGCCAGC
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
US-09-864-761-6005
                                                                                                                                                                                                                                                                                                                                                 Score 132.2; DB 10; Length
Pred. No. 1.2e-22;
0; Mismatches 138; Indels
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWAKE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 6005
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                                                                                                                                                                   MAP TO AC006070.1
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Patent No. US20020081607A1
                                                                                                                                                                                                                                                                                                                                                   Query Match 12.0%;
Best Local Similarity 62.6%;
Matches 241; Conservative (
                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                  FEATURE:
OTHER INFORMATION:
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US-09-874-062-2/C
                                                                                                    LENGTH: 464
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL PO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ETILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-06-26
PRIOR FILING DATE: 2000-08-03
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                                                                                    93 CGGCCAGGAGGATGCTGCCCCCCAGCTGCTGCCAGACCACCTGCTGCTGCAGGACCACCTG 152
                                                                                                                                                                                                                    665 CAGC/FGAAAGGGCAGCGGCAGC/FGGACACACAGCAGCTGGGATGACAGC/PAGAAA/FG 606
                                                                                                                                                                                                                                                            213 CTGCAAACCCAGCTGCTGCCTGACCACCTGCTGCAGGACCACCTGCTGCCGCCAAAAATG 272
                                                                                                                                                                                                                                                                                                                                                 333 CTGCAGGACCACCTGCTGCCGCCCCAGCTGCTTTCCAGTTGCTGCAGGCCTTCCTG 392
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                                                                                                                               725 CAGCAAGAACTGCCGCAGCAGATGGGGTGGAAGCAGGTTGTTCTACAGCAGGTGGTGGTGGG
                                                                                                                                                                           153 CTGCCCCCCCCCCCCTGCTGCATTTCCAGTTGCTGCAGCCTTCCTGCTGTATCTCCAGCTG
                                            0
  Length 1101;
Score 129; DB 10;
Pred. No. 1.3e-21;
0; Mismatches 315;
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  11.7%;
50.2%;
                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCA 358
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NN: EXPRESSED IN HT444, SIGNAL = 1.9

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3

NN: EXPRESSED IN BOUT LIVER, SIGNAL = 2

NN: EXPRESSED IN BONE MARROW, SIGNAL = 2

NN: EXPRESSED IN LUNG, SIGNAL = 1.6

NN: EXPRESSED IN HACKENTA, SIGNAL = 1.5

NN: EXPRESSED IN HELOW, SIGNAL = 1.3

NN: EXPRESSED IN HELOW, SIGNAL = 1.5

NN: EXPRESSED IN HELOW, SIGNAL = 1.5

NN: EXPRESSED IN HELOW, SIGNAL = 1.5

NN: EXPRESSED IN HELA, SIGNAL = 2.2

NN: EXPRESSED IN HEAT', SIGNAL = 2.2

NN: EXPRESSED IN H
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52.4%; Pred. No. 4.8e-21;
Live 0; Mismatches 268; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICK FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 2486
                                                                                                                                                                                               TELING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00669

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00668

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00663

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00661

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: US 60/234,687

OR APPLICATION NUMBER: US 60/234,687

OR APPLICATION NUMBER: US 60/234,687

OR PAPLICATION NUMBER: US 60/234,687

OR PILING DATE: 2000-06-30
                                                                                                                         FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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FILING DATE: 2001-01-29
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APPLICANT: Chen, wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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GCTGCTGCATTTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCA 418
                                                                                                                                               GCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCATTTCTAGTTGCTGCAGGCTTT 478
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60.718
PRIOR PELING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-09-39
PRIOR PELING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-37
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
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; Sequence 22070, Application US/U9864761
; Patent No. US20020048763A1
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NN: EXPRESSED IN HEART, SIGNAL = 1.9

NN: EXPRESSED IN LUNG, SIGNAL = 1.9

NN: EXPRESSED IN HELA, SIGNAL = 1.9

NN: EXPRESSED IN HELA, SIGNAL = 1.9

NN: EXPRESSED IN BRAIN, SIGNAL = 1.9

NN: EXPRESSED IN BRAIN, SIGNAL = 1.9

NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

NN: EXPRESSED IN HTT: P4591, EVALUE 1.50e+00

NN: EXT. HUMAN HTT: BE350684 1, EVALUE 2.00e-05

NN: NT HIT: M27685.1, EVALUE 2.00e-17
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEC ID NO 22070
LENGTH: 364
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Matches 236; Conservative
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ORGANISM: Homo sapiens
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Compugen Ltd.
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US-09-258-A-2

US-09-359-081-2

US-09-130-114-1

US-08-130-114-1

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US-09-620-925-1

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US-09-620-925-1

US-08-081-94-088-15

US-08-194-088-15

US-08-194-088-15

US-09-010-9288-1

US-09-330-371A-20

US-09-230-371A-20
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US-08-056-200-93
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              GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvitus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS TELECOMMUNICATION INFORMATION: TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                 US-09-010-928B-1
US-08-425-069-3
US-08-317-844B-3
US-09-370-838-157
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US-08-209-747-1
US-08-458-298-1
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US-08-864-038A-2
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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STRANDEDNESS: single
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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RESULT 3
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SEQ ID NO 1
LENGTH: 348
TYPE: DNA
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APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REPERBENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PALENTING DATE: 1998-11-19
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                                  CAGCTCCTGCTGTGGCTCTGTCTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGA
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  1.7e-42;
ches 295;
             Mismatches
  NO.
  Pred.
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  59.38;
             429; Conservative
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  Local Similarity
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                                                        Length 3489;
                                                                                          Mismatches 295;
 sarcoma-associated herpesvirus
                                                      Score 252; DB 4;
Pred. No. 1.7e-42;
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Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Edelman, 1sidore S.
APPLICANT: Edelman, 1sidore S.
APPLICANT: Moore, Patrick S.
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; ORGANISM: Kaposi's
US-09-298-568-1
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POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
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Pred. No. 3.2e-42;
0; Mismatches 295; Indels 0
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 59.3%;
Matches 429; Conservative
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                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                   New York
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                                                                                                                                              ZIP: 10036
                                                                   ADDRESSEE:
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Pred. No. 3.2e-42;
0; Mismatches 295; Indels 0
                                                                                                                                                                                     TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentln Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/757,669
Sequence 20, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Hobenzky, Roy A.
APPLICANT: Kusso, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Rober Patrick S.
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 451
TELECOMMUNICATION INFORMATION:
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TELEFAX: (212) 391-0525
INPORMATION FOR SEQ ID NO: 20: 20: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 59.3%;
Matches 429; Conservative (
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EDNESS: double
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                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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RY: U.S.A.
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APPLICANT: Bohenzky, Roy A
APPLICANT: Busco, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Gelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SAKCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: UNBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
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US-09-230-371A-20
Sequence 20, Application US/09230371A
Patent No. 6348586
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                                                                42 CAGCTCCTGCTGTGGCTCTGTTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGUCCAGGA
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                                 Gaps
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Patent No. 6417002
GENERAL INFORMATION:
GARAL INFORMATION:
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT PILING DATE: 1999-02-11
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Score 252; DB 4; L. Pred. No. 3.2e-42; 0; Mismatches 295;
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 22.9%;
59.3%;
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US-09-249-585A-2/c
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                                                     Length 1926;
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                                                                            Indels
                                                     Score 167.4; DB 4;
Pred. No. 2e-25;
0; Mismatches 336;
: LOCATION: (1)..(1926)
; OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09050863 Patent No. 6114111 GENERAL INFORMATION:
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APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mamma
TITLE OF INVENTION: Systei
                                                                           Matches 382; Conservative
                                                                  Similarity
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SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 2.2e-25;
); Mismatches 336;
                                                                      ADDRESSEE: Flehr, Hohbach, Test, Albritton
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
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MEDIUM TYPE: Florpy disk
COMPUTER: IHM PC COMPALIBLE
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53.0%;
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INFORMATION FOR SEQ ID NO: 2:
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REGISTRATION NUMBER:
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EDNESS: unknown
                                     CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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US-09-050-863-2
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Best Local Simi
Matches 382;
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COUNTRY:
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Pred. No. 2.7e-25;
); Mismatches 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09130114
Patent No. 5976807
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Cobbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Ex
TITLE OF INVENTION: Eukaryotic Transfected
FILE REFERENCE: 0867/10903US1
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SOFTWARE: FastSEQ for Windows Version 3.0
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53.0%;
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Matches 382; Conservative
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LENGTH: 5452
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US-09-130-114-1
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                             ATTTCTAGTTGCTGTCATCCCAGCTGCTGTGTCTCAGCTGCCGCTGCCCTTTCAGCTGC
                                                                                                                          CCGACCACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCAGTTCTTGCTGC
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ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert STREET: & Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                               Hiang, Betty
Payan, Don
TITLE OF INVENTION: Don
System
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WINDER READABLE FOORM:
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/050,863
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/COCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,70,70,70)
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Pred. No. 2.2e-25;
0; Mismatches 336;
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FILING DATE: 22-Jul-1999
CLASSIFICATION: <UNKNOWN>
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TYPE: nucleic acid
STRANDEDNESS: unknown
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09359081 Patent No. 6316223 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lao, Ying
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GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
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Patent No. 6251433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy disk
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US-08-910-647-1/C
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 Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                               Score 167.4; DB 4;
Pred. No. 3.2e-25;
0; Mismatches 336;
                                                                                                          NAME: Fujita, Sharon M.
REGIGSTRATION NUMBER: 38,459
REERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923.2706
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                     APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                 15.2%;
53.0%;
                                                       FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             : 9600 base pairs
nucleic acid
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SOFTWARE: Patentin Re CURRENT APPLICATION DATA
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Best Local Similarity
Matches 382; Conserv
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487 ATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCCAACTGTTGT 546
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                 307 ATCTCCAGCTGCTAGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 18M PC compatible of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
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TELEPHONE: 415/225-3216
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                             STATE: CALIFORNIA

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94680-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: TBM PC COMPATIBLE

COMPUTER: TBM PC COMPATIBLE

COMPUTER: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/620,925

FILING DATE: 21-Jui-2000

CLASSIFCATION SURNOWN>

PRIOR APPLICATION DATA:
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                                                                                                                                                                                                 TITLE OF INVENTION: Compositions and Methods for Polynucleotide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: FUJITA, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-620-925-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/910,647
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (510) 923-2706
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                                                                                                                           Sequence 1, Application US/09620925
Patent No. 6468986
                                                                                                                                                                                   APPLICANT: Zuckermann et al
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                   CITY: Emeryville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382; Conservative
                                                                                                                                         Patent No. 6468986
GENERAL INFORMATION:
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                                  T 726
T 727
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Best Local :
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Sequence 15, Application US/07885971
Fatent No. 5128837
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS: NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                247 AGGACCACCTGCTGCCCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGT
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                                                                                          AGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCCTGACCACCTGCTGC
                                                                     Gaps
                                             Length 10596;
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Pred. No. 3.3e-25;
0; Mismatches 336;
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                             Ouery Match
Best Local Similarity 53.0%;
Matches 382; Conservative
 single
            ; 'TOPOLOGY: linear
US-07-884-811-15
STRANDEDNESS:
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53.0%; Pred. No. 3.3e-25;
Live 0; Mismatches 336;
                                                                          5.25 inch, 360 Kb floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,971
FILING DATE: 19920518
                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                           15:
                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                  415/952-9881
                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
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Best Local Similarity
Matches 382; Conservat
California
                                                                                                            OPERATING SYSTEM:
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                     COUNTRY:
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                                                                                                                                     247 AGGACCACCTGCTGCCCCCCAGCTGCTTTTCCAGTTGCTGCAGGCTTTCCTGCTTGT 306
127 CAGACCACCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGC 186
                                                                                      427 AGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCTAGTTGCTGCAGGCCTTCCTGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie K. TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VAKIANTS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: 5.25 inch, 360 Kb floppy disk
IRM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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GENERAL INFORMATION:
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APPLICATION NUMBER: 07/884811
FILING DATE: 18 MAY-1992
ATTORNEY/AGENT INFORMATION:
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607 ATTICTAGTIGCTGTCATCCCAGCTGCTGTGTGTCCAGCTGCCGCTGCCCTTTCAGCTGC
                                                                                                    667 CCGACCACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCAGTTCTTGCTGC
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FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 167.4; DB 1; Length 10596;
Pred. No. 3.3e-25;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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0; Mismatches
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APPLICANT: GOGOWSKI, Paul J., Lokker, Nair TITLE OF INVENTION: HEPATOCYTE GROWTH FAA.
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/087,783A FILING DATE: 13-Jul-1993
                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08087783A
Patent No. 5547856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-Jul-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/885971
FILING DATE: 18 - MAY - 9.
ATTORNEY/AGENT INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,600
REPERBUCK/DOCKET NUMBER: PO7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
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ilarity 53.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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les 382; Conserva
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US-08-087-783A-15/C
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US-08-087-783A-15
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Best Local S
Matches 382
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Job time : 81

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1111 | 1 | 1 | 1|1 | 1 | 1|1 | 1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.2%; Score 167.4; DB 1; Length 10596; 53.0%; Pred. No. 3.3e-25; Live 0; Mismatches 336; Indels 3;
                                                                                 755D1
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 755D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-2614
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEOUBNCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 53.0
Matches 382; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-194-088B-15
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Search completed: June 18, 2003, 15:49:23

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(without alignments)
7629.077 Million cell updates/sec
                                                                                                                                                               June 18, 2003, 03:06:50; Search time 325 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                  Run on:
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US-09-874-062-2 1101 Perfect score: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

2185239 seqs, 1125999159 residues Searched:

4370478 Total number of hits satisfying chosen parameters:

Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0%

N_Geneseq_101002:* Database :

1: /SIDS2/gcgdata/geneseqn-emb1/Na1980.DAT:*
2: /SIDS2/gcgdata/geneseqn-emb1/Na1981.DAT:*
3: /SIDS2/gcgdata/geneseqn-emb1/Na1981.DAT:*
4: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1981.DAT:*
5: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1984.DAT:*
6: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1985.DAT:*
7: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1985.DAT:*
8: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1986.DAT:*
9: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1989.DAT:*
10: /SIDS2/gcgdata/geneseqy-emeseqn-emb1/Na1989.DAT:*
11: /SIDS2/gcgdata/geneseqy-geneseqn-emb1/Na1989.DAT:*
12: /SIDS2/gcgdata/geneseqy-geneseqn-emb1/Na1991.DAT:*
13: /SIDS2/gcgdata/geneseqy-geneseqn-emb1/Na1991.DAT:*
14: /SIDS2/gcgdata/geneseqy-geneseqn-emb1/Na1991.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* /SIDS2/gcgdata/geneseq/genesegn-cmbl/NA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT: DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993. 15: 16: 17: 18: 20: 0:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human cDNA clone H	DNA encoding novel	Human polynucleoti	Human polynucleoti	Kaposi's sarcoma-a	Nucleotide sequenc	Kaposi's sarcoma-a	KSHV LUR DNA (nucl	KSHV long unique c
	QI	AAD06303	AAS93555	AAK52135	AAK53119	AAA30290	AAF82901	ABA93487	AAV73805	AAV19941
	DB	22	23	22	22	21	22	24	20	13
	Watch Length DB ID	1101	627	1851	1851	3489	3489	3489	32207	137507
	Match	100.0	47.4	25.3	25.3	22.9	22.9	22.9	22.9	22.9
	Score	1101	521.4	278.6	278.6	252	252	252	252	252
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198 18.0 461 22 AAKO8838 198 18.0 461 22 AAK131470 198 18.0 461 22 AAK31470 198 18.0 461 22 AAK31470 187 15.0 2108 24 ABL66774 167.4 15.2 1926 22 AAF82902 167.4 15.2 2580 21 AAA50324 167.4 15.2 2580 21 AAA50323 167.4 15.2 2580 20 AAX3178 167.4 15.2 2580 20 AAX3178 167.4 15.2 10580 20 AAX23778 167.4 15.2 10596 14 AAA50513 167.4 15.2 10596 14 AAA5183 167.4 15.2 10596 14 AAA5183 167.4 15.2 10596 14 AAA5183 167.4 15.2 10596 20 AAX15650 167.4 15.2 10596 20 AAX15650 167.4 15.2 10596 20 AAX15650 167.4 15.2 10596 20 AAX15650 167.4 15.0 489 22 AAK18627 165.4 15.0 489 22 AAK18627 160.2 14.6 478 22 AAK3034 160.2 14.6 478 22 AAK3034 160.2 14.6 478 22 AAK3134 160.2 14.6 478 22 AAK3134 160.2 14.6 478 22 AAK3186 160.2 14.6 478 22 AAK3184 160.2 14.6 478 22 AAK3184 160.2 14.6 478 22 AAK313874 160.2 14.6 478 22 AAK31387 160.2 14.6 478 22 AAK31387 160.3 14.6 478 22 AAK31387 160.2 14.6 478 22 AAK31387 160.3 14.6 478 22 AAK3188 160.3 14.6 478 22 AAK3188 160.3 14.6 478 22 AAK3188 160.3 14.6 47	13	198	Э.	9	22	ABA57772	foetal
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Location/Qualifiers Homo sapiens Key

/*tag* a //product= "Human four disulfide core domain (FUCD)-containing protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases (e.g. neoplasms of the breast or liver), hyperproliferative disorders (e.g. neoplasms of the breast or liver), cardiovascular disorders (e.g. cardiac arrest), cerebrovascular disorders (e.g. cardiac arrest), nervous system disorders (e.g. cerebral ischaemia, angiogenesis), nervous system disorders (e.g. Alzheimer's disease), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infection). The FDD-containing proteins are used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. They are used in diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological symptoms associated with the disorders and in diagnostic immunossays
                                                                                                                                                                                                                                                                                     The present sequence is human cDNA clone HWHQC55 encoding four disulfide core domain (FDCD)-containing protein. FDCD sequences are used to prevent, treat or ameliorate skin disorders such as congenital disorders e.g. moles, freckles and haemangiomas as well as integumentary tumours (keratosis, basal cell carcinoma, malignant melanoma), injuries and inflammation of the skin, atherosclerosis, urticaria, eczema, photosensitivity, autoimmune disorders (lupus erythematosus, scleroderma), keloids, striae, erythema, petechiae, purpura and xanthelasma. They are also used in the diagnosis and treatment of diseases and disorders of hair and epithelium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGAGGCTGCTGCCGCCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGCCAGACCACCTGCTGCAGGACCACCTGCTGCTGCCCCCAGCTGCTGCATTTCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGGAACCCACCCAGAACCTCCACCTCTGACGCCATGGTCAGCTCCTGCTGTGGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTGCTCTGACCAGAGCTGTGGTCAAGGTCTCGGCCAGGAGGTGCTGCCGCCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radioimmunoassays or enzyme linked immunosorbent assays (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Four disulfide core domains (FDCD) containing polypeptide and its polynucleotide are used to prevent, treat or ameliorate a medical condition associated with FDCD e.g. skin disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1101 BP; 220 A; 343 C; 231 G; 307 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1101; DB 22;
Pred. No. 2.7e-194;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .g. radioimmunoassays or enzyme illured imministration in PDCD sequences are also used in gene therapy.
                                                                                                                                                                                                                                                             Claim 1; Page 229; 235pp; English.
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ilarity 100.0%;
Conservative 0
                                                       2000WO-US32462
                                                                                                            (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                 2001-356153/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                      Shi Y;
                                                                                                                                                                              -PSDB; AAE02058
WO200140249-A1
                                                      29-NOV-2000;
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Matches 1101;
                           07-JUN-2001
                                                                                                                                      Ruben SM,
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GTATCAATTTTCATGTGGAATTGTTTGATGTTCCTCAATAAAACTTCATAGTGTTCAAAA 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTGCTGAGTGAAGGTGCTCTGGATTTGTGCACCTTCTTGCTCTCAAGCTTTGAGTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTGATTTGGAAAATATTTATTAGTATGTATTCTCTTTTATAGAAGTTTTTATTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACAGAGTATCTATTCAGAGACATGTGGACTTCCTGATGTCGTGAAAACAGAGGCATG
                                                                                                                                                                                           TGCTGCAGGACCACCTGCTGCCCCCAGCTGCATTTCTAGTTGCTGCAGGCCTTCC
                                                                                                                                             AGCTGCCCGACCTGCTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCAGTTCT
TGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCCAGC
                                                                TGCTGCATTTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCTGCAAGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed gones. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in capporatics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human call and polynucle data for this patent did not appear in the printed sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTICCTGCTGTATCTCCAGCTGCAAACCCAGCTGCTGCCTGACCACCTGCTGCAGGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACCTGCTGCCGCCCCAGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGCTGCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCCAGCTGCTGCAGGA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 627 BP; 89 A; 240 C; 151 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 521.4; DB 2;
Pred. No. 2.6e-87;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 29359; 103pp; English.
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llarity 91.5%;
Conservative
                                                                                                             2000US-0540217.
2000US-0649167.
                                                                 30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
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es 552; Conserv
                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                      P-PSDB; ABG29368
                                                                                                                                     23-AUG-2000;
                                                                                                               31-MAR-2000;
                   11-0CT-2001
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW18323-AAM80302) that exhibit activity elating to cytokine, cell prollferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or
                                                                                       019
                                                                                                                                                                                                                                                                             CCACCTUCTTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGGCGCAGTTCTTGTTGTTGAG 730
                                                                                                                                                                                                                                                                                                      therapy;
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                                                                                                                                                                                                            CTAGCTGTTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCAGCTGCTGTATCT
                        CTAGTTGCTGTCTCTCCCAGCTGCTGTGTGTGCAGCTGCCGCTGCCCTTTCAGCTGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u P, Xu C, Ca
Chen R, Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYSE , ...-
Tang YT, Liu C, Drmanac RT, Asundı v, -
" Wanq D, Wang J, Zhang J, Ren F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2374-2376; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful in diagnosis and yene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ 1D NO 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK52135 standard; cDNA; 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0496914.
2000US-0560875
2000US-0590075.
2000US-0654936.
2000US-0654936.
2000US-0658561.
2000US-0693325.
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20-OCT-2000;
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20-JUN-2000;
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us-09-874-062-2.rng

Human; cytokine; cell proliferation; cell differentiation; gene throaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

2000US - 0496914. 2000US - 0560875. 2000US - 0598075. 2000US - 0629325. 2000US - 0654936. 2000US - 063561. 2000US - 0693561.

01-SEP-2000; 15-SEP-2000; 20-OCT-2000;

30-NOV-2000;

20-JUN-2000; 19-JUL-2000; 03-FEB-2000; 27-APR-2000;

2001WO-US04098

05-FEB-2001;

09-AUG-2001

WO200157190-A2.

Homo sapiens.

Human polynucleotide SEQ ID NO 2648

06-NOV-2001

AAK53119;

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peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                          2111 (AAK52582) and 3666 from the sequence listing
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                                                                                                                                                                               Sequence 1851 BP; 379 A; 558 C; 574 G; 340 T; 0 other;
                                                                                                                                                                                                                  25.3%; Score 278.6; DB 22;
65.7%; Pred. No. 2.3e-42;
iive 0; Mismatches 224;
                                                                                                        Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                           were missing at the time of publication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GUTGTGGTCAAGGTCTCGGCCAGGAGGTGCTGCCGCCCCCAGGTGCTGCCAGACCACT
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Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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AAK53119 standard; cDNA; 1851 BP

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                                                                                                                                                    270 CCTGCCGCCCCAGCTGTGTGTGTCCAGCTGCTGCCGTCCACTCTGCTGTCAGACCACCT 1329
039 GTTGCTGCCCCAGCTGTGTTGTATCCAGCTGCTGCCGCCCATCCTGCTCTCAGACTACCT 1098
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                                                                                            317 GCTGCAAACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCTATTCCAGTT 376
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                  GCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCTGACCACCTGCTGCAGGACCACCT
                                                       GCTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human immunodeficiency virus; HIV; multicentric Castleman's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lateucy-associated nuclear antigen; LANA; gamma-2 herpes virus;
Human herpes virus 8; HHVB; rhadino virus cis-acting element; RVCAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "nuclear localisation signal, NLS"
190..210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "nuclear localisation signal, NLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaposi's sarcoma-associated herpesvirus LANA gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaposi's sarcoma; primary effusion lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (aposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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The Process of the American associated nuclear antique (LANA) gene. KSHV is a second and belongs to the rhadino virus, or as Human Herpes Virus 8 (HHV8) and belongs to the rhadino virus, or againa-2 herpes virus class. The LANA protein is necessary for file efficient persistence of rhadino virus bnA in mammalian cells. Persistent cardino virus infection is implicated in a variety of diseases e.d. Kaposi's Sarcoma (KS), Primary Effusion Lymphoma (PEL) and multicentric castleman's disease. In addition, KS is a common malignancy in HIV parists in host cells in a latent form One of the few genes expressed from the latent viral DNA is LANA. LANA associates with comes expressed from the latent viral DNA is LANA. LANA associates with the RACE, thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the host chromosomes. This allows the viral DNA to persist in the heavy child the rhadino virus careen and identify molecules that inhibit LANA interaction with RVCAE, thereby interfering with the latency cycle of this virus. Potential antiviral trealments for the above mentioned diseases may therefore be based on LANA dereyulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the Kaposi's sarcoma-associated herpesvirus
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99US-0298568
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Best Local Similarity 59.3°
Matches 429; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Ballestas ME,
                                                                                                                                                                                                                                          (KIEF/) KIEFF E D.
(BALL/) BALLESTAS M
(KAYE/) KAYE K M.
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P-PSDB; AAY96255.
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                                                                                                                                       19-NOV-1998;
21-APR-1999;
                                                                     19-NOV-1999;
25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                            tethering protein; LANA; gene therapy; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition for use in gene therapy comprises an expression vector at includes a nucleic acid sequence encoding a nucleic acid binding
                                                                                                                                         TAGTTGCTGCAGGCCTTCCTGCTGTATCTCTAGCTGTTGCAAACCCAGCTGCTGCCAGAC
                            CACCTGCTGCCGCCCCAGCTGCTGTATCTCCAGCTGCTACAGGCCCCAGTGCTGCCAGCC
                                                                CTCCTGCTGCCGCCCGGCTTGCTGCATTTCTAGTTGCTGTCATCCCAGCTGCTGTGTGTC
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                                                                                                                                                                   CATCTGCTGCGGCAGTTCTTGCTGCTGAGTGAAGCTGCTCTGGATTTGTGCACCTTCTTG
                                                                                                                                                                                                                                                                                                                                                           Parkinson's disease; Huntington disease; diabetes; human herpesvirus KSHV; latency-associated nuclear antigen; LANA; ds.
                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of KSHV tethering protein, LANA
                                                                                                                                                                                                                                                                                                                                                                                        Kaposi's sarcoma associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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ID AAF82901 standard; DNA; 3489
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P-PSDB; AAB62331.
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protein suitable for tethering DNA to Histone H1. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone H1 and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis. Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Kaposi's sarcoma
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                                                                                                                                                                                                                                                                                       Length 3489;
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                                                                                                                                                                                                                                          Sequence 3489 BP; 1053 A; 862 C; 1137 G; 437 T; 0 other;
                                                                                                                                                                                           antigen (LANA), which acts as a tethering protein.
                                                                                                                                                                                                                                                                                                                                         295;
                                                                                                                                                                                                                                                                                          Score 252; DB 22;
Pred. No. 2.2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSHV LUR DNA (nucleotides 105, 301-137,507).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a system (A) for maintaining a plasmid as an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigen) of 3489 base pairs (see ABA93487, S1) expressed in the cell, and the rhadinoviral sequence (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, S2) present in the plasmid Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having (S2) as a cis-acting and maintenance sequence in the DNA. (A) is particularly used in gene therapy (or other gene transfer applications) that uses mammalian cells in which LANA is expressed. (A) improves persistence of gene therapy vectors in cells. The present sequence encodes Kaposi's sarcoma-associated herpesvirus (KSHV, also called human herpesvirus 8) LANA protein, which is used in the exemplification of the
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0
                                                                                                                              Kaposi's sarcoma-associated herpesvirus; KSHV; LANA; RVCAE; PE KSHV terminal repeat; rhadino virus cis acting element; episom primary effusion lymphoma; latency-associated nuclear antigen; gene therapy; gene transfer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       System for episomal retention of plasmids in mammalian cells, gene therapy, comprises rhadinoviral LANA and RVCAE sequences
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                                                                                                                                                                                                                                                                                                                                                                                          /note= "latency-associated nuclear antigen"
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                                                                                     Kaposi's sarcoma-associated herpesvirus LANA protein
                                                                                                                                                                                                                                                                                                                                                                "LANA protein"
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1..3489
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                                                                                               herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF69, KI2 which encodes kneedes a glycoprotein, ORF73 which encodes immediate early protein (IEP), K14 which encodes (cyclin D), ORF73 which encodes immediate early protein (IEP), K14 which encodes (cyclin D), ORF74 which encodes tegument protein/FGARAT, K15. KSHV is a new human encodes tegument protein/FGARAT, K15. KSHV is a new human most common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's
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di.hydro:folate reductase and is useful for treatment, prophylaxis
or diagnosis of Kaposi's sarcoma
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                                                                                      sequence is a fragment of the Kaposi's sarcoma-associated
                                                                                                                                                                                                                                                                                                                                                                              22.9%; Score 252; DB 20; Length 32207;
larity 59.3%; Pred. No. 3.6e-37;
Conservative 0; Mismatches 295; Indels 0;
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                                              Disclosure; Column 155-182; 109pp; English.
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es 429; Conserv
                                                                                                                                                                                                                                                                                                               sarcoma in a cell
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interleukin-6; II-6; Interferon regulatory factor; rheumatory protein II; complement-binding protein; dytooprotein; dytooprotein; daysoprotein; dytooprotein; dytooprotein; dytooprotein; dytooprotein; kaposi's sarcoma; protective vaccine; lymphoproliferative disease; leukaemia; splenomegaly; myroosis lunqoides; HIV immune status; anti-infiammanery access.
                                                                                                                                                                 HHV8; human herpes virus 8; macrophage inflammatory protein 11;
                                                                                                                                                                                                                                                                                                                                                                                                      /product= macrophage inflammatory protein 11
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/product* interferon regulatory factor 1
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complement (17261..17875)
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                                                                                                                                                                                                                                                                                                                                                                                complement (21548..21832)
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                                                                                                                                                                                                                                              Kaposi's sarcoma-associated herpes virus
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762 CTCT 765
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cytokine; cell proliferation; cell differentiation; growth factor;
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                                                                                    402 CAGCTGCTGCAAACCCAACTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCTTTC
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known as human herpes virus 8 (HHVB). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral interleukin 6 (IL-6); (c) viral IRF]. (d) complement-binding protein: glycoproteins B, M or L; (d) capsid protein IV encoded by ORFF3. Eabelled probes for the nucleic acid, proteins encoded by orFF3. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for detecting HHVB. specifically for diagnosis of Kaposi's sarcoma, in body (inids or tissue samples. HHVB infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the cortism. Ab may be used for prophylaxis or treatment of HHVB infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHVB may be implicated in many other lymphoproliferative diseases such as lymphomas, leukaemia.

Con their lymphoproliferative diseases such as lymphomas, leukaemia.

Splenomegaly and mycosis fungoides. Cells and animals containing the nucleic acid are useful for drug screening. HHVB derived peptides can be used as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methotrexate. These can also be used to determine the immune status of a patient infected with HVV. HHVB derived protein viral MIP III may be used as an anti-inflammatory agent for, france of a patient infected with HVV. HWB derived protein for e.g. the immune status of a patient infected with HVV. HWB derived protein for e.g. the immune status of a patient infected with HVP. HWB derived protein for e.g. the immune status of a patient infected with HVP. HWB derived protein for e.g. e.g. the treating the treating the treating the treating the tre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 GAGCTGCTGCCGCCCCAGCTGCTGCCAGCCTGCTGCAGGACCACCTGCTGCCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 CAGCTGCTGCTTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 CAGCTGCTGCTGACCACCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                     virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 22.9%; Score 252; DB 19; Length 137507; Local Similarity 59.3%; Pred. No. 5.1e-37; es 429; Conservative 0; Mismatches 295; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding Kaposi's sarcoma associated herpes proteins – useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                                                                                                                                                                                                                                                                                                   Russo JJ;
                                                                                                                                                                                                                                                                                                                   Moore PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 135-203; 230pp; English.
                                                                                                                                                                                                                                                                                                                 Edelman IS,
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                                                        960S-0686243.
960S-0686349.
960S-0686350.
960S-0687253.
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96US-0747887.
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97WO-US13346
                                                                                                                                                                96US-0708678
                                                                                                                                                                                                                                                                                                               Chang Y,
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                                                                                                                                                                                                                                                                                                                 Bohenzky RA,
22-JUL-1997;
                                         29-NOV-1996
                                                                                25-JUL-1996;
                                                                                                     25-JUL-1996;
                                                                                                                         25-JUL-1996;
                                                                                                                                              25-JUL-1996;
                                                                                                                                                                05-SEP-1996
                                                                                                                                                                                        10-0CT-1996
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                                                                                                                                                                                                                                 13-NOV-1996
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Contribution also relates to vectors and recombinant nost ceits comprising a nucleotide of the invention, methods of producing the novel polypeptides, contribodies against the polypeptides, methods of detecting the novel polypeptides or polypeptides and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have been been proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activity; is negatively; laematopolesis regulatory activity; tissue growth activity; laematopolesis regulatory activity; tissue growth activities; chemotactic or chemokinetic activity; activin. or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis concitions, e.g., by protein or gene therapy. Such conditions include concitions, e.g., by protein or gene therapy. Such conditions include disorders, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., myeloid or lymphoid cell cepair (or nucleic acids encoding them) may be used to promote wound crepair (or nucleic acids encoding them) may be used to promote wound cepair includes may be used to promote very partities may be used in the treatment of viral, batterial and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used to promote vells manipulate to give rise to neuroepithalial cells in culture to give rise to neuroepithalial cells in culture to give rise to neuroepithalian cells in culture to give rise to neuroepitalian cells and anomar or repeated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                    Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGCTCTGACCAGAGCTGTGGGTCAAGGTCTCGGCCAGGAGGTGCTGCTGCCGCCCCAGCT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 TGAAAACCCACCCAGATCCTCCCCGTTCTGACACCATGGTCACTCTGTTGTGGCTCCG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                             Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 101; Indels
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                                                                                                                                                                                                                                     Claim 1; Page 977; 1963pp; English.
  Tang YT, Liu C, Drmanac RT;
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Matches 297; Conservative
                                                                                                                                                                                 e.g. arthritis and cancer
                                                   2001-457740/49.
                                                                            P-PSDB; ABB12277
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, varcines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arUnitis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of cancer, leukaemia, nervous system disorders, arthritis and
Inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
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                              302 GCTGTATCTCCAGCTGCTACAAACCCAGCTGCTGCAGGACCACCTGCTGCTGCCGCCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities,
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Wang ?
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Chen R,
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                                                                                         362 GCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATC 399
                                                                                                                      373 GCTGTGAGACGACCTGCCACCCTANGTGCTGCATC 410
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', Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2374-2376; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO 680.
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Yang Y, Wejhrman T,
                                                                                                                                                                                                     AAK52135 standard; cDNA; 1851
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2000US-0598075.
2000US-0620325.
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2000US-0663561.
2000US-0693325.
2000US-0728422.
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                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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20-OCT-2000;
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(HYSE-) HYSEQ INC.
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                                                                                                                                                        Yang Y,
                                                                                                                                     Liu C,
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                                                                                                                                              Wang
                                                                               15-SEP-2000; 20-OCT-2000; 30-NOV-2000;
                                  03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                05-FEB-2001;
                                                             19-JUL-2000;
01-SEP-2000;
09-AUG-2001
                                                                                                                                     Tang YT,
Zhao QA,
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                                                       1200 CTGCTGCCAGCCTTGCTGCCACCCAACTTGCTGTCAAAACACCTGCTGCAGGACCACCTG 1259
                                                                                                                               1377 CTGTCAGCCTATTTGTGGGTCCAGTTGCTGTCAGCCTTGCTGTCACCGGACTTGCTATCA 1436
                                                                                                                                                                                                                                         GAACACCTCTTGCCAGCCCACCTGCTGTGGGTCCAGCTGCTGCCGCCACCCTTGCTGCTGCCACCC 1556
                                                                                                                                                                                                                                                                                                                   677
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                                                                                                                                                       CTGCAAACCCAGCTGCTGCTGACCACCTGCTGCAGGACCACCTGCTGCCGCCCCCAGCTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human: cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                             92
                                                                                                                                                                                            CTGCATTTCCAGTT-----GCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTAA
                                                                                                                                                                                                                                ACCCAGCTGCTGCAGGACCACCTGCTGCCCCCCAGCTGCTGCATTTCCAGTTGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTCATCCCAGCTGCTGTGTGTCCAGCTGCCGCTGCCCTTTCAGCTGCCCGACCACCTG
                                                                                                                                                                                                                                                                                                        444 CCCCAGCTGCTGCATTTCTAGTTG-----CTGCAGGCCTTCCTGCTGTATCTCTAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                CTACAGGCCCCAGTGCTGCCCAGCCCTCCTGCTGCCGCCCGGCTTGCTGCATTTCTAGTTG
                                                                                93 CGGCCAGGAGAGCTGCTGCTGCCCCCAGCTGCTGCCAGACCACCTGCTGCAGGACCACCTG
                                                                                                                    CTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTG
                                             33 CGCCATGGTCAGCTCCTGCTGTGGCTCTGTCTGCTCTGACCAGAGCTGTGGTCAAGGTCT
                           Gaps
                           21;
       Length 1851;
                        258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGG 713
                4.5e-28;
                           0; Mismatches
        Score 201.2;
Pred. No. 4.5
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        18.3%;
59.9%;
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                 al Similarity 59.9
417; Conservative
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        Query Match
Best Local S
Matches 417
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encoded polypeptides (AAM/8132AAM/80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypublides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAAACCCAGCTGCTGACCACCTGCTGCAGGACCACCTGCTGCTGCCGCCCCAUCTG 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCATTTCCAGTTGCTGCAG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTTCCTGCTGTATCTCCACCTGCTGCAAACCCAGCTGCAGGACCACCTGCTGCTGCG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCAGCCCA---CTTGTGTGGCCAGCTGCTGCCTGCTTCCTGCAGCACACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 CGCCATGGTCAGCTCCTGTGTGTGTCTGTCTGACCAGAGCTGTGGTCAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides with cytokine-like activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and
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                                                                                                                                                                                                                                                                                                                                                                         J C,
Wang ?
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                                                                                                                                                                                                                                                                                                                                                                                  χu,
                                                                                                                                                                                                                                                                                                                                                                            Wang J, Zhang J, Ren F, Chen Wejhrman T, Goodrich R;
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0; Mismatches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in diagnosis and gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT,
                                                                            2000US-0560B75.
2000US-0598075.
2000US-0620325.
2000US-0654936.
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2000US-0693325,
2000US-0728422.
2001WO-USU4098
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121 160 181 241 280 301

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                                                                                                                                                                                    122 GCTGCCAGACCAGCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTGCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; ephlepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 5829.
Sequence 461 BP; 74 A; 171 C; 107 G; 109 T; 0 other;
                                             Pred. No. 1.3e-z/,
0; Mismatches 115;
                               198; DB 22;
No. 1.3e-27;
                                Score 198;
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2000US-0234687.
2000US-0236359.
                               Query Match 18.0%;
Best Local Similarity 71.2%;
Matches 306; Conservative
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                       Proce: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                  CCCCAGCTGCTGCATTTCTAGTTG-----CTGCAGGCCTTCCTGCTGTATCTCTAGCTG
                                                                                 295 AACATGCTGTCAAACCATTTGTAGATCCACCTGCTGCCAACCATCCTGTGTGACCAGATG
                                                                                                                  TTGCAAACCCAGCTGCTGCCAGACCACCTGCTGCCGCCCCAGCTGCTGTATCTCCAGCTG
                                                                                                                                                                                    CTACAGGCCCCAGTGCTGCCAGCCCTCCTGCTGCCGCCCGGCTTGCTGCATTTCTAGTTG
                                                                                                                                                                                                                                                  CTGTCATCCCAGCTGCTGTGTCCAGCTGCCGCTGCCCTTTCAGCTGCCCGACCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #6077.
                                                                                                                                                                                                                                                                                                                    CTGTAGAACAACCTGCTTCCACCCCATCTGCTGCGG 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                      Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157277-A2
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26 MAY - 2000; 2
30 - JUN - 2000; 2
03 - AUG - 2000; 2
21 - SEP - 2000; 2
27 - SEP - 2000; 2
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completed: June 18, 2003, 10:20:21
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                                                                                                                                                                                                                                                                                                                                                                 301
                                                                         probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                          expression in human
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                                                                  The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression analysis; probe;
                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed single exon probe SEQ ID NO: 6027.
                                                                                                                                                               Score 198; DB 22; Length 461;
Pred. No. 1.3e-27;
0; Mismatches 115; Indels
                                                                                                                                                                                    Indels
                                              ID NO: 5829; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                              Sequence 461 BP; 74 A; 171 C; 107 G; 109 T; 0 other;
                  probes for analyzing gene
                                                                                                                                                                 18.0%; Score 198;
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Conservative
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                  Single exon nucleic acid
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|GCTGTCAGAC 461
WPI; 2001-483446/52
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                                                                                                                                                                          Similarity
                                                Example 4; SEQ
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bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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Pred. No. 1.3e-27;
0; Mismatches 115; Indels
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                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human bone marrow
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71.2%;
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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30-JAN-2001; 2001WO-US00668
                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                                               Chen
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Best Local Similarity 71.29
Matches 306; Conservalive
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                                                     26-MAY-2000;
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03-AUG-2000;
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27-SEP-2000;
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Sequence 281, Appl
Sequence 281, App
Sequence 39564, A
Sequence 43621, A
Sequence 283, App
Sequence 283, App
Sequence 135, App
Sequence 135, App
Sequence 337, App
Sequence 381, App
Sequence 381, App
Sequence 47, Appl
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Sequence 37946, A
                                                                           June 11, 2003, 11:05:01 ; Search time 45 Seconds (without alignments) 527.672 Million cell updates/sec
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1484
1 WVSSCGSVCSDQSCGQGLG......PTTCCRTTCFHPICCGSSCC 230
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/cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-864-761-37946

US-10-123-155-147

US-10-123-155-99

US-10-184-644-281

US-10-184-644-281

US-09-864-761-39564

US-09-864-761-39564

US-10-184-644-283

US-10-184-644-283

US-10-184-64-135

US-10-184-64-135

US-10-184-64-135

US-10-184-64-135

US-10-184-64-135

US-10-184-64-135

US-10-184-64-135

US-10-184-64-135

US-10-123-155-193

US-10-123-155-193

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US-10-184-64-47
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Maximum Match 100%
Listing first 45 summaries
                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTON:
TITLE OF INVENTON: POLYPEPLICES, and Antibodies
FILE REFERENCE: PT033P1
CORRENT APPLICATION NUMBER: US/09/874,062
CORRENT PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US00/32462
PRIOR APPLICATION NUMBER: 60/168,229
PRIOR FILING DATE: 1999-12-01
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                         US-10-184-644-467

US-10-184-644-469

US-10-184-644-499

US-10-184-644-593

US-10-184-644-593

US-10-184-644-299

US-10-184-644-289

US-10-184-644-287

US-10-184-644-287

US-10-123-155-67

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US-10-123-155-67

US-10-123-155-67

US-10-175-737-581

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; Patent No. US20020081607A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
Best Local Sim
Matches 230;
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LENGTH: 230
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120

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KPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCC 120

61

61 KPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCC

121 ISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQCC 180

121 ISSCCKPSCCRTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRQCC

QPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCCRTTCFHPICCGSSCC 230

181

181 QPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCRTTCFHPICCGSSCC

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2953 CCTTCC----CGTGTGTCTTCC---CCCTGCCAAGCCTCCCCTGCCAAGCCTCCCTG 3005
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                                                                                                                                                                                                                                                              89 CCISSCCKPSCCRTTCCRPSCLISSCCRPSCCISSCCKPSCCRTTCCRPSCCLS-----S 143
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                                                                                                                      88
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                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30
                                                                                                                   29 CCQTTCCRTTCCRPSCC1SSCCRPSCC1SSCCKPSCCLTTCCRTTCCRPSCC1SSCCRPS
                                                                                                                                                                                                                                                                                                                                             144 CCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQCCQPSCCRPACCISSCCHPSC----
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                                                           20; Gaps
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     Length 231;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - See Palm or File Wrapper
  34.6%; Score 513; DB 10;
40.6%; Pred. No. 2.4e-26;
ive 29; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 -CVSSCRCPFSCPFFCCRFFCFHPICCGSSCC 230
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CURRENT FILLING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 147, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sherwood, Steven
Smith, Victoria
Query Match
Best Local Similarity 40.65
Matches 86; Conservative
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang, Zemin
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ORGANISM: Homo Sapien
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APPLICANT:
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                                                                                                                                                                                                                                      APPLICANT: HORSEL, DAVIG K.
TITLE OF INVENTION: HUMAN CRNONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT APPLICATION: HUMAN EXER: US/09/864,761
CURRENT PLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/04/10/312
PRIOR APPLICATION NUMBER: US/04/20/456
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-06-27
PRIOR PRIOR FILING DATE: 2000-06-359
PRIOR PRIOR PRIOR FILING DATE: 2000-06-27
PRIOR PRIOR PRIOR FILING DATE: 2000-09-27
PRIOR PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR PRIOR 2001-01-30
PRIOR PRIOR PRIOR SECURITION NUMBER: PCT/0501/0663
PRIOR PRIOR PRIOR PRIOR 2001-01-30
PRIOR PRIOR PRIOR 2001-01-30
PRIOR PRIOR PRIOR PRIOR 2001-01-30
PRIOR PRIOR PRIOR 2001-01-30
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NI. EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

NI. EXPRESSED IN DULT LIVER, SIGNAL = 1.9

NI. EXPRESSED IN BOUT LIVER, SIGNAL = 1.3

NI. EXPRESSED IN BONE MARROW, SIGNAL = 2

NI. EXPRESSED IN LUNG, SIGNAL = 1.6

NI. EXPRESSED IN PLACENTA, SIGNAL = 1.7

NI. EXPRESSED IN HELA, SIGNAL = 1.3

NI. EXPRESSED IN HELA, SIGNAL = 1.3

NI. EXPRESSED IN HELA, SIGNAL = 1.5

NI. EXPRESSED IN HELA, SIGNAL = 2.2

NI. EXPRESSED IN HERAT, SIGNAL = 2.2
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SOFTWAKE: Annomax Sequence Listing Engine vers. 1.1
                                                                                     Sequence 37946, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAP TO AC003958.1
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                        US-09-864-761-37946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 37946
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RESULT 6
US-10-184-634-281
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Best Local S
Matches 97
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                  99 CCRTTCCRPSCCISS------CCRPS------CCISSCCKPSCCRTTCCRPS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 RPQCC------QPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCRTTCFHPICC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...-CY 175
QT---TCCR----PSCCISSCYRPQCC---QPSCCRPACCISSCCHPSCCVSSCRCPFSC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1904;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.3%; Score 479.5; DB 9; 30.8%; Pred, No. 1.1e-23; ive 22; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SSCCGSVCSDQSCG-----QGLGQESCCRPSCCQTTCC-
                                                                                             3179 AGGTAACGCCACTAATCAGGCAGGGGCC 3206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/123,155 CURRENT FILING DATE: 2002-04-15
                                                             211 P-----TTCCRTTCFHPICCGSSCC
                                                                                                                                                                        Sequence 99, Application US/10123155 Publication No. US20030068794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                         Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                          Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                      Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 30.8
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                        Goddard, Audrey
                                                                                                                                                                                                                                                         DeForge, Laura
                                                                                                                                                                                                                                                                                                        Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKGANISM: Homo Sapien
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 CTTCCTGCCC -- TCCTTTCCTGCCC -- ACGCCTGCTTCCTGCCCTTCTCCGAGCCCTT 167
                                                                                     APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Andrey
APPLICANT: Goddard, Andrey
APPLICANT: Goddard, Andrey
APPLICANT: Gordowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Mood, William I.
APPLICANT: Anany Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEUC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 ---SCCISSCCRPSC----CISSCCRPSCCLTTCCRTTC--CRPSCCIS--SCCRPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 CTAGGAGGAGG--TCCFGGGGTCTGFGGGTTGATCTGTGGCCCCTGFGCCPFTGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 CQPSCCRP-ACCISSCCHPSCCVSSCRCPFSCPTTCCRTTCFHPICCGSSCC 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CCGSVCSDQSCGQGLGQESCCRPSCCQTTC----CRTTCCRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ 1D NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.3%; Score 479; DB 9;
33.2%; Pred. No. 1.1e-23;
iive 27; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 281, Application US/10184634; Publication No. US20030068684A1; GENERAL INFORMATION:
Sequence 281, Application US/10184644 Publication No. US20030044930Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe, Colin K.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: P3430R1C217
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Inc
APPLICANT: Goddard, Andrey
APPLICANT: Goddwski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 33.2 97; Conservative
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Smith, Victoria
                                                                          APPLICANT: Baker, Kevin P.
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ORGANISM: Homo Sapien
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSP-CCQPTCCRTTCWKPT------TVTTCSSTPCCQPSCCVSSC 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N: EXPRESSED IN PLACENTA, SIGNAL = 2.4

N: EXPRESSED IN HEART, SIGNAL = 2.2

N: EXPRESSED IN BRAIN, SIGNAL = 2.5

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5

N: EXPRESSED IN LUNG, SIGNAL = 2.5

N: EXPRESSED IN HELA, SIGNAL = 2.5

N: EXPRESSED IN HELA, SIGNAL = 2.5

N: EXPRESSED IN HELA, SIGNAL = 2.5

N: EXPRESSED IN HETA, SIGNAL = 2.4

N: SWISSPR(X) HIT: P02438, EVALUE 7.40e-02
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PRIOR APPLICATION NUMBER: PCT/USU1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
SEQ ID NO 99564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatches
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CURRENT FILING DATE: 2001-05-23
PRIOR PELLCATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-07
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Patent No. US20020048763A1
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.0°
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 COPSCCRP-ACCISSCCHPSCCVSSCRCPFSCPTTCCKTTCFHP1CCGSSCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACI
TITLE OF INVENTION: GNE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                               32.3%; Score 479; DB 9; Length 1732; 33.2%; Pred. No. 1.1e-23; tive 27; Mismatches 72; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                     5 CCGSVCSDQSCGQGLGQESCCRPSCCQTTC----CRTTCCRP---
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
LENGTH: 1732
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                            : ORGANISM: Homo Sapien
US-10-184-634-281
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 97; Conserv
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US-09-864-761-39564
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29.9%; Score 443; DB 9;
31.5%; Pred. No. 2.5e-21;
tive 20; Mismatches 85
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; Sequence 283, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
          Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Matches 96; Conservative
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                                                             Zhanq, Zemin
                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo Sapien
US-10-184-644-283
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GGACC 611
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LENGTH: 2294
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          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.2%; Score 448; DB 10; Length 102; 51.3%; Pred. No. 2e-22;
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11; Mismatches 14; Indels
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OR APPLICATION NUMBER: PCT/USO1/00665

OR PILING DATE: 2001-01-30

OR FILING DATE: 2001-01-30

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00663

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00662

OR APPLICATION NUMBER: PCT/USO1/00661

OR FILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00661

OR PILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00670

OR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00664
PRIOR FLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PRIOR DATE: 2000-09-21
PRIOR PRIOR DATE: 2000-09-30
PRIOR PLING DATE: 2000-09-30
                            APPLICATION NUMBER: PCT/USO1/00667 FILING DATE: 2001-01-30 PAPLICATION NUMBER: PCT/USO1/00664 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/USO1/00669
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Matches 77; Conservative
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APPLICANT: Chen Jian
APPLICANT: Chen Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Fun, Jamey, Austin L
APPLICANT: Smith, Victoria
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Smith, Victoria
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ORGANISM: Homo sapiens
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SCCRTTC-----CRPSCCISSCCRPSCCISSCCKPSCCQTTC-----CRPSCCISSC 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 CRPSCC--ISSCCKPSCCLITT-------CR-TTCCRPSCCISSCRPSC 89
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RT227 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 283 LENGTH: 2294
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TITLE OF INVENTION: SECRETED AND TRANSMEWBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEO ID NOS: 612
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ORGANISM: Homo Sapien
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250 GCGCC--GCC--TCCACGCCCTCCTTCTCC----CCTGGCCGGGC---GCCTGGTACTCGG 299
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                                                                250 GCGCC--GCC--TCCACGCCCTCTTCTC---CCTGGCCCGGC---GCCTG();2A3;3GG 299
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  190 GETTCCTGCCCCCCCGCBAACCCCCGAGGTCACCAGCCCGCGCCTCTGCTTCCCTGGGCCGCCCCCA49
                                       153 --SCCKPSCCQTTCCRPSCCISSCYRPQCCQPSCCRPACCISSCCHPSCCVSSCKC--- 206
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: 105/10/184,634
CURRENT FILING DATE: 2002-06-28
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                                                                                                                   207 PFSCPTT----CCRTTCFHPIC----CGSSCC 230
                                                                                                                                                           300 GACCGTTGCCTGACGCGAGGCCCAGCTCTACTTTCGCCCC 340
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32.4%; Pred. No. 5e-21;
.ive 12; Mismatches 108;
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Sequence 543, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION: APPLICANT: Haker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Publication No. US20030068684A1
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Watanabe, Colin K.
Wood, William 1
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Godowski, Paul J.
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Best Local Similarity 32.49
Matches 91; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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US-10-184-634-135
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US-10-184-634-135
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LENGTH: 2651
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                      145 AGGCGCCGCTCGCCCTCGCCGACCACCCC - TCCGGCGGGGGAACGCACTTCGACC - 500
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                                                                                                                                                                                                                                                                                                                                                                                                                       175 YRPQCCQPSCCRPACCIS----SCCHPSCCVSSCRCPFSC-PTTCCRTTCFHPICC 225
                                                                                                                                                                                                                                                            ----CISSCCKPSCCRTTCCRPSCCISSCCRPSCC------ISSCCKP 127
                                                                                                                                      133 ACCGGGCC-CCCGCGCGCCCACCGTCCACCGACCCCTGCGACTTCTCCAGCCCAGTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wood William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CCGSVCSDQSCG-QGLGQE-----SCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCC
                                                                                                   SCCGSVCSDQSCGQGLGQESCCRP--SCCQTTCCRT------TCCRPSCCISSC
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                                                         85; Indels 104; Gaps
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Pred. No. 5e-21;
2; Mismatches 108; Indels 70;
                b; Score 443; DB 9; Length 2294;
b; Pred. No. 2.5e-21;
20; Mismatches 85; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 135, Application US/10184644 publication No. US20030044930A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith,Victoria
Watanabe,Colin K.
Query Match
Best Local Similarity 31.55
Best Local Similarity 31.55
For 96; Conservative
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ORGANISM: Homo Sapien
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US-10-184-644-135
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Gerritsen Mary E.
Goddard, Audrey
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Sherwood, Steven
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Gao, Wei-Qiang
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Best Local Similarity 29.99
Matches 93; Conservative
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; ORGANISM: Homo Sapien
US-10-123-155-337
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                                                                                                                                                                                             APPLICANT: Wood, William APPLICANT: Zhang, Zemin TTTLE OF INVENTIONS SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30 CURRENT APPLICATION NUMBER: US/10/123,155 CURRENT FILING DATE: 2002-04-15.
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Publication No. US20030068794A1
GENERAL INFORMATION:
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
                                                Gerritsen, Mary E.
Goddard, Audrey
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Watanabe, Colin K
Wood, William
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                                                                                 Godowski, Paul J.
Gurney, Austin L.
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Desnoyers, Luc
Filvaroff, Ellen
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
                                                                                                                               Smith, Victoria
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US-10-123-155-543
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33304HC30
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P33304LG30
CURRENT APPLICATION NUMBER: 105/10/123,155
CURRENT FILLING DATE: 2002-04-15
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                                                                                                                                                                Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 337
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CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or Fi
SEQ 1D NO 381
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Query Match 29.4%; Score 437; DB 9; Length 2236; Best Local Similarity 32.2%; Pred. No. 6e-21; Matches 89; Conservative 9; Mismatches 110; Indels 68; Gaps 16;
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                                                                                                                                                         5 CCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSC 64
                                                                                                                                                                             40 CCGGCCTGCGCCCCCGCCCC--GCGCGCCCCCCCAACC----CCGGCCCGCGC 94
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-381
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OM protein - protein search, using sw model

June 11, 2003, 11:02:46 ; Search time 22 Seconds (without alignments) 433.616 Million cell updates/sec Run on:

US-09-874-062-3
1484
1 WASCCGSVCSDQSCGQGLG......PTTCCRTTCFHPICCGSSCC 230 Title: Perfect score: Sequence:

Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ptio	075690 homo sapien	P08131 ovis aries	71 homo	3 ovis	0 ovis	9 ovis	2 ovis	capra	P02443 ovis aries	P02441 ovis aries	P14728 xanthomonas	P15265 mus musculu	P11976 dictyostel		homod		mus m						_	P22105 homo sapien		P34504 caenorhabdi	Q01705 mus musculu	9/	Q25464 mytilus gal	2	_	P31695 mus musculu
SUMMARIES		ID	KRUB_HUMAN	KR2D_SHEEP	KRUA_HUMAN	KR2A_SHEEP	KR2C_SHEEP	KR2B_SHEEP	KRUC_SHEEP	KRA3_CAPHI	KR3A_SHEEP	KRA3_SHEEP	YAV2_XANCV	MCS_MOUSE	PSTA_DICDI	STC_DROME	NFX1_HUMAN	SREC_HUMAN	ZAN_MOUSE	NTC3_HUMAN	FUR2_DROME	NTC1_HUMAN	NTC3_RAT	NTC4_HUMAN	NTC3_MOUSE	TENX_HUMAN	YNC3_YEAST	YMV2_CAEEL	NTC1_MOUSE	BAR3_CHITE	FP2_MYTGA	VWF_HUMAN	YLK3_CAEEL	NTC4_MOUSE
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		Score	465	434	420.5	408.5	358.5	348	305.5	284	279	269.5	224.5	221.5	217.5	210	198	194	184.5	1	82	81	180.5	78	74	74	173	173	-	171.5	171	9	168	168
	Result	NO.	-	2	٣	4	ស	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32

ratius norv	drosophila	home sapien	sus serofa	mus muscala	r grannlins	qallus qall	ratins norv	homo sapien	branchiosto	brachydanio	canis famil
001008	P02840	P24821	028833	004592	P23785	P10039	08w30	004721	Q9n j 15	P46530	028295
NTC1_RAT	SGS3_DROME	TENA_HUMAN	VWF_P1G	PCK5_MOUSE	GRN_RAT	TENA_CHICK	NTC2_KAT	NTC2_HUMAN	PCK5_BRACL	NTC1_BRARE	VWF_CANFA
	-	_	_	_	_	-	-	_	_	_	_
			۰.	7	20	30	_	_	'n	7	٠٠.
2531	307	2201	2482	187	28	180	247	247	169	243	281
. •		11.0 2201	•	_			•	•		•	•
11.2	11.0	. •	11.0	11.0	10.9	10.8	10.8	10.7	10.6	10.6	10.6

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between the Swiss Institute of Bioinformatics and the FMBL outstation—the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/annonnec/
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                 ---- C 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGHD MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR MOLECULAR WEIGHTS OF 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SSCCGSVCS--DQSCGQGLGQESC-----CRPSCCQTTCCRTTCCRPSCCISSCCRPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perez C., Auriol J., Gerst C., Hernard B.A., Egly J.-M.; "Genomic organization and promoter characterization of two human HHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAIR FOLLICLES.

DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.

DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                    Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McKinnon P.J., Powell B.C., kopers G.E.; "Structure and expression of genes for a class of cysteine-rich proteins of the cuticle layers of differentiating wool and hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.3%; Score 420.5; DB 1; Length 169; ilarity 46.3%; Pred. No. 6.8e-28; Conservative 13; Mismatches 56; Indels 25.
112 CRPDCRVEGTSLPPCCVVSCTSPSCCQLYYAQASCCRPSYCGQSCCRPAC-
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Multigene family.
169 AA: 16276 MW: 219814FEEB49D4AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99148005; PubMed 10023044;
Perez C., Auriol J., Gerst. C., Bernard B.A.,
                                                                                                                                                                                                               169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                      163 COPTCIEPVC-----EPTCCEPTC 181
                                                              160 COTTCCRPSCCISSCYRPOCCOPSC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91115951; PubMed-1703541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Cell Biol. 111:2587-2600(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA07189.1;
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:6409; KRN1.
MIM; 148021; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X55293; CAA39005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keratin genes.";
Gene 227:137-148(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RICH (SR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X33227,
AJ006693; CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Follicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                 KRN1 OR UHSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01064;
                                                                                                                                                                                                                  KRUA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                follicles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keratin; F
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 CRPSCCISSCCRPSCCISSCCKPSCC----RTTCCRPSCCISSCCRPSCCISSCCKPSC 159
                 RTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCC 160
                                        26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83299218; PubMed-6193483;
MEDLINE-83299218; PubMed-6193483;
Powell B.C., Sleigh M.J., Ward K.A., Rogers G.E.;
"Mammalian Keratin gene families: organisation of genes coding for the B2 high-sulphur proteins of sheep wool.";
Nucleic Acids Res. 11:5327-5346(1983).
-! FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERWAH, DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULPUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SCCG-SVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCCKP
                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoslomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.2%; Score 434; DB 1; Length 181; 37.1%; Pred. No. 5.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D3E4874E21757B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X 10 AA TANDEM REPEATS.
                                                                                                                             152 QSSCCKPCCCSSGC-GSSCCQSSCCKPCCSQSSCCVPICC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 SCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSC----
                                                                                                    QTTCCRPSCCISSCYRPQCCQPSCCRPACCISSCCHPSCC
                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
Keratin, high-sulfur matrix protein, B2D.
                                                                                                                                                                                                                                                        181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002494; Keratin_B2.
                                                                                                                                                                                                                                                                                              08, Created)
08, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01500; Keratin_B2; 1.
Keratin; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X01610; CAA25759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KERATINS (40-56 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Caprinae; Ovis. NCBI_TaxID=9940;
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
35
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85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S07911; KRSHHD.
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nes 76; Conserv
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                                                                                                                                                                                                                                                     KR2D_SHEEP
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DOMAIN
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                                                                                                    161
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REPEAT
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KR2D_SHEEP
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                                                             111
                             CISSCCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 kDa)
SGCCGSSCGCCDSSCG-----SCGSGCRGCGPSC----CAPVYCCKPVC----CCVPAC
                                                  SCSSCGRRGCGSCGGSKGCGSCGCSQCSCCRP-CCCSSGCGSSCCQCSCCKPYCSQCSC
                                                                                                      112 CKP-CCSSGRGSSCQSSCCKP-CCSSGGGSSCCQSSCCKPCCSQSRCCVPVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elleman T.C.; The aminon acid sequence of protein SCMK-B2A from the high-sulphur fraction of wool keratin "; Biochem. J. 130:833-845(1972).
                                                                                                                                                                                                                                 1-JUL-1986 (Rel. 01, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
Keratin, high-sulfur matrix protein, B2A.
Evis arises (Sheep).
Evisaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Mori a... Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                             Powell B.C., Sleigh M.J., Ward K.A., Rogers G.E.; "Mammalian keratin gene families: organisation of genes coding for the B2 high-sulphur proteins of sheep wool."; Nucleic Acids Res. 11:5327-5346(1983).
                                                                                        CRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCKPSCCOTTCCRPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: THE SOURCE OF THIS KERATIN IS LINCOLN WOOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> T (IN MINOR COMPONENT).
-> N (IN MINOR COMPONENT).
-> F (IN MINOR COMPONENT).
79290B74A1B9044C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                   171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 408.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=83299218; PubMed=6193483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=73224964; PubMed=4679226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002494; Keratin_B2.
Pfam; PF01500; Keratin_B2; 1.
                                                                                                                                                                                                                              (Rel. 01, Created)
(Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X01610; CAA25757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keratin; Acetylation;
INIT_MET 0 0 0 MOD_RES 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02837; KRSHHA
PIR; S07910; S07910
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 AA;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9940;
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36
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22
23
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21-JUL-1986 (
01-AUG-1991 (
                                                                                                                                                                                                KR2A_SHEEP
                                                          53
                                                                                        115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                              P02438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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                                                                                                                                                                                  KR2A_SHEEP
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                   7
                                                                                                              SCCLTTCCRTTCCRPSCC1SSC-----CRPSCC1SSCCKPSCCRTTCCRPSCC1S 112
                                                                                                                                           TSIQTSCCQPTCLQTSGCETGCG1GGS1GYGQVGSSGAVSS-----RTRWCRPIN:RVF 109
                                                                                                                                                                            SCCRPSCC1SSCCRPSCC----RTTCCRPSCC1SSCCRPSCC1SSCCKPSCCGTTTCTRP 167
                                                                               56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 GTSLPPCCVVSCTPPSCCOLIYYAGASCCRPSYCGOSCCRPAC------CCOPTCLEP
                                                                 1 ACCSTSFGGFPICSTG----GTGGSSPCOPTCCQTSCCQPTSIQTSCCQPISIQTSGCQD
                                               4 SCCG-SVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCCKP
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EuteleosLowi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83299218; PubMed-6193483; Powell B.C., Sleigh M.J., Ward K.A., Rogers G.E.; Mammalian keratin gene families: organisation of genes coding for the B2 high-sulphur proteins of sheep wool."; Nucleic Acids Res. 11:5327-5346(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: THE SOURCE OF THIS KERATIN IS LINCOLN WOOL.
                58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04258F835696F186 CRC64;
   6.3e-27
                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 0], Created)
01-AUG-1988 (Rel. 08, last sequence update)
01-AUG-1991 (Rel. 19, last annotation update)
Keratin, high-sulfur matrix protein, B2C.
                                                                                                                                                                                                                                                                                                                                                      151 AA.
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETY LAI'T JON
   Pred. No.
                                                                                                                                                                                                                                           SCCISSCYRPQCCQPSCCRPAC 189
                                                                                                                                                                                                                                                                       -----ICEPSCCEPFC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=72077141; PubMed=5289313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002494; Keralin_B2.
Pfam; PF01500; Keratin_B2: 1.
Keratin; Acetylation; Repeat.
                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
ME
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 37.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
15475
                   Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
36
46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elleman T.C.;
                                                                                                                                                                                                                                                                                                                                                      SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                              63
                                                                                                                                                                            113
                                                                                                                                                                                                                                           168
                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                       KESULT 5
KR2C_SHEEP
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NOT THE PROPERTY OF THE PROPER
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                                                   'n
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                                                                                                                                                                                                                           61 GGSTGYGQVGSSGAVSSRTRWCRPDCRVEGTSLPPCCVVSCTSPSCCQLYYAQASCCRPS 120
                                                                                                                                                                                   -----CRITCCRPSCCISSCCRPSCCISSCCKPSCC-----RTTCCRPS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCCQTTCCR-TTCCRPSCCISSCCRPSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCR 86
                                                                                                                                 1 ACCSTSFCGFPICSTAGTCGSSCCRSTCSQTSCCQPTSIQTSCCQPTCLQTSGCETGCGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elleman T.C., Dopheide T.A.;

"The sequence of SCMK-B2B, a high-sulfur protein from wool keratin.";
J. Biol. Chem. 247:3906-3906-19072).

SUCH AS WOOL AND HAIR PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR AND HIGH-TROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 kDa, WHERRAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCSTSFCGFPICSSVGTCGSSCGQPTCSQTSCCQP----TSIQTSCCQPISIQTSCCQ
                                                                                         43 SCCISSCCR-PSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSC--
                                                 39; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC----RTICCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 CCISSCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQCCQPSC 184
                                                                                                                                                                                                                                                                                                121 YCGQSCCRPAC-----CQQPTCTEPVC-----EPTCSQPIC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.5%; Score 348; DB 1; Length 156
Best Local Similarity 37.3%; Pred. No. 4.3e-22;
Matches 62; Conservative 23; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D -> G (IN MINOR COMPONENT).
EE549ADCF1F1FB39 CRC64;
                                                 Indels
                                                 46;
    DB 1;
  Score 358.5; DB 1
Pred. No. 6.1e-23;
18; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-AUC-1991 (Rel. 19, Last annotation update)
61-AUC-1991 (Rel. 19, Last annotation update)
Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
MEDLINE=72206034; PubMed=4555954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02838; KRSHHB.
InterPro; IPR002494; Keratin_B2.
Pfam; PF01500; Keratin_B2: 1.
Keratin; Acetylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 AA; 16040 MW;
  24.2%;
38.0%;
                                            63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                         Similarity
                                                                                                                                                                                 100 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                       KR2B_SHEEP
Query Match
Best Local S
Matches 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
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REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                             KR2B_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GKGGG-SSCGGSKGGCGSCGGSKGGCGSCGKPVC----CCVPACSCSKGKG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCISSCCKPSCCRPTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCC1SSCYRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GCGSCGGSKGGGSKGGGSKGGCGSCCVPVC----CCVPACSCSSCGKG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SSC---CGSVCSDQSCGOGLGQESCCRPSCCQTTCCRTTCCRPSCCTSSCCRPSCCTSSC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Cell Biol, 111:2587-2600(1990).

-!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGHD MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULEUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 KDa, WHEREAS THE MICROFIGRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 KDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.
-i- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
                                                                                                                                                                                Ovis aries (Sheep).
Wakaryota: Metazoa: Chordata: Craniata: Vertebrata; Eutheries: Mammalia; Eutheria: Cetartiodactyla: Ruminantia: Pecora: Rovoidea: Bovidae: Caprinae: Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                McKinnon P.J., Powell B.C., Rogers G.E.; "Structure and expression of genes for a class of cysteine-rich proteins of the cuticle layers of differentiating wool and hair follicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                      01-AuG-1992 (Rel. 23, Greated)
01-AuG-1992 (Rel. 23, Last sequence update)
15-Jun-2002 (Rel. 41, Last annotation update)
Keratin, ultra high-sulfur matrix protein (UHS keratin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9BDD4901FCB13295 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AA.
182 AA
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keratin; Repeat; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91115951; PubMed=1703541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCCQPSCCRPACC1SSCCHPSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AA; 16101 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X55294; CAA39006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 38.9
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S'TANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RICH (SR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A36686; A36686.
HSSP; P02876; 9WGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOOL FOLLICLES.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
KRUC_SHEEP
P26372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID KRA3_CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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us-09-874-062-3.rsp

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KRA3_SHEEP
                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keratin.
                                                            Keratin
                                                                                                                                                                                                                                                                      RESULT 10
KRA3_SHEEP
                                                                                                             Matches
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SYNDRUCCO
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                                                                                                                                                                                                                                                                                                                                                                                                                             63 SCCLTTCCRTTCCRPSCCISSCCRP-SCCISSC----CKPSCCRTTCCRPSCCISSCCRP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Swart L.S., Haylett T.;

"Studies on the high-sulphur proteins of reduced Merino wool. Amino acid sequence of protein SCMKB-343.";

Blochem. J. 133:641-654(1973).

"FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
                                                                                                                                       SCCGPTFSSLSCGGGCLQPRYYRDPCCCRPVSCQTTVSRPVTFVSRCTRP-----ICEP
                                                                                                                                                                                                                                                                                                                                                                          4 SCCGSVCSDQSCGQGLGQESCCR-PSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCCKP
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                  19.1%; Score 284; DB 1; Length 132; 40.1%; Pred. No. 5.5e-17;
      21-JUC-1986 (Rel. 01, Created)
21-JUC-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Keratin, high-sulfur matrix protein, IIIA3 (M2.6 protein).
                                                                                                                                                                                                                                                                                                  MISSING (IN MINOR COMPONENT).
6COCC8BFA13AB28B CRC64;
                                                                                                                                                                                                                                                                                                                                                       56; Indels
                                                                                                                                                                                                                                                                                          Y -> C (IN MINOR COMPONENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Last sequence update) 01-AUG-1991 (Rel. 19, Last annotation update) Keratin, high-sulfur matrix protein, IIIA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AA.
                                                                                                                                                                                                                                                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCISSCCKPSCCRTTCCRPSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=74022242; PubMed=4584026;
                                                                                                                                                                                                                                                        InterPro; IPR002494; Keratin_B2. Pfam; PF01500; Keratin_B2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                              132 AA; 14255 MW;
                                                                                                                       STRAIN=South African angora;
                                                                             Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                        23
                                                                                                                                  Joubert F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KR3A_SHEEP
                                                                                                             SEOUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                Keratin
                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P02443;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCLTTCCRTTCCRPSCCISSCCRP-SCCISSC----CKPSCCRTTCCRPSCCISSCRPS 118
                                                                                                                                                                                                                                                                                                                                                                                  23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SCCGPTFSSLSCGGG-----CLOPRYYRDPC----CCRPVSC-OTVSRPVTFVPRCTRPL 52
                                                                                                                                                                                                                                                                                                                                 4 SCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCCKPS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SCGGPTFSSI,SCGGG-----CLQPCCYRDPC----CCRPVSSTQTVSRPTFVSRCTRP1
6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 kDa).
-!- MISCELLANEOUS: THE SOURCE OF THIS KERATIN IS MERINO WOOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swart L.S., Haylett T., "Studies on the high-sulphur proteins of reduced Merino wool. Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
Keratin, high-sulfur matrix protein, flIA<sup>3</sup>.
0vis aries (Sheep)
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetarliodactyla; Ruminantia; Pecora; Bovoidea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANEOUS: THE SOURCE OF THIS PROTEIN IS MERINO WOOD...
                                                                                                                                                                                                                               18.8%; Score 279; DB 1; Length 130; 39.5%; Pred. No. 1.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 AA; 14163 MW; 8C0B56C0070B1C50 CRC64;
                                                                                                                                                                                130 AA; 13894 MW; 8ACF3719FBBB8361 CRC64;
                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%; score 269.5; DB 138.3%; Pred. No. 7.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.2%; Score 269.5; Best Local Similarity 38.3%; Prod. No. 7.9e Matches 54; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 CCISSCCKPSCCRTTCCRPSCCISSCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 SC-----PSAPKTTC--KTFKTSPCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 CCISSCCKPSCCRTTCCRPSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=74022242; PubMed=4584026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002494; Keralin_B2.
                                                                                                     InterPro; IPR002494; Keratin_B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01500; Keratin_H2; 1.
                                                                                                                            Pfam; PF01500; Keratin_B2; 1
                                                                                                                                                                                                                                                                                58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Caprinae; Ovis.
                                                                                  PIR; A02841; KRSH3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02840; KRSHA3.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9940;
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                                    -----SCCISSCYRPQCCQP-----SCCRP----ACCISSCCHP--- 197
                                                                                                               527 LAMATICSGVRPWAWHSTGNSACIVSSACLPPILLAMATICSGVRPWAWHSTGNSRCTVS 586
                                                                                  --SCCVSSCRCP---FSCPTTC--CRTTCFHPI----CCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-33039675; PubMed=1418626; Karimpour I., Cutler M., Shih D., Smith J., Kleene K.C.; Sequence of the gene encoding the mitochondrial capsule aselmoproretin of mouse sperm: identification of three in-phase TGA selenocysteine codons."; DNA Cell Biol. 11:693-699(1992).
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 221.5; DB 1; Length 197; 33.9%; Pred. No. 7.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kleene K.C., Smith J., Rozorgzadeh A., Harris M., Hahn L.,
Karimpour I., Gerstel J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A37199; A37199.
MGD; MGI:96945; Mcsp.
Mitochondrion; Selenium; Selenocysteine; Sperm; Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21015 MW; 721B84F7129F02B1 CRC64;
                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sperm mitochondrial capsule selenoprotein (MCS).
                                                                                                                                                                                                                                                                    197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90152148; PubMed-2303168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M88463; AAB08438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 55-197 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M29603; AAA53045.1; -.
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                  SCC 230
                                                                                                                                                                                    SAC 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                        MCSP OR MCS.
                                                                                                                                                                                                                                                                MCS_MOUSE
P15265;
                                                                                                                                                  228
                                                                                                                                                                                    587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                  198
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                                                                                                                                                                                                                                                      MCS_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 MATTCCGVRPWAWHSTGNSRCTVSS-----ACLPPSWLAMATTCSGVRPWAWHSTGN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 WAWHSTGNSRCTVSSACLPPSWLAMA--TTCSGVRPWAWHSTGNSRCTVSSACLPPSWLA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SCCISSCCKPS---CCRTTC--CRP------SCCISSC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 CRP------ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 CLPPLLLAMATTCSGVRPWAWHSTGNSRCTVSSACLPPPLLAMATTCCGVRPWAWHSTGN 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 -SCCISSCCRP-----CRP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 SRCTVSSACLPPSWLAMATICSGVRPWAWHSTGNSRCTVSSACLPPSWLAMATICSGVRP 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΒY
                                                                                                                                                                                                                                                                                                                                                                  avrBs3 from Xanthomonas campestris pv. vesicatoria.";
Mol. Gen. Genet. 218:127-136(1989).
-!- DISEASE: THE TERM AVIRULENT DESCRIBES A POTENTIALLY VIRULENT
PATHOGEN WHICH IS UNABLE TO INDUCE DISEASE SYMPTOMS IN SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                   CULTIVARS OF PEPPER.
-!- MISCELLANEOUS: THIS IS ONE OF THE HYPOTHETICAL PROTEINS CODED THE OPEN READING FRAMES WITHIN THE REGION REQUIRED FOR AVRBS3
                                                                                                                                                                                                                                                                                                STRAIN=Isolate 71-21;
MEDLINE=89384426; PubMed=2550761;
Bonas U., Stall R.E., Staskawicz B.;
"Genetic and structural characterization of the avirulence gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSCCG-----SVCSDQSCGQGLGQESCCRPS--CCQTTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267;
                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%; Score 224.5; DB 1; Length 784; 22.6%; Pred. No. 9.1e-12; ive 19; Mismatches 88; Indels 267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 82 kDa avirulence protein in AVRBS3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---CRTTCC--RP-----SCCISSCCRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3B2624B411793744 CRC64;
                                                                                  784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR005042; Avirulence.
Pfam: PF03377; Avirulence; 1.
Hypothetical protein: Plasmid; Virulence.
SEQUENCE 784 AA; 82074 MW; 3B2624B411;
                                                                                                                                                                                    Xanthomonas campestris (pv. vesicatoria).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16130; -; NOT_ANNOTATED_CDS.
PIR; JQ0317; JQ0317.
111 SCQPAPCSRTTCRTFRTSPCC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 22.6
109; Conservative
                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                  NCBI_TaxID=341;
                                                                                                                                                                                                 Plasmid pXV11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY.
                                                                                                                                                                                                                                   Xanthomonas
                                                                                  YAV2_XANCV
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Matches 10
                                               RESULT 11
YAV2_XANCV
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     15;
                                                                                                                                                     129
                                                                                                                                                                                                                                               130 CRTTC---CRPSCCISSCCRPSCCISSCCKPSCCQTTCC-RPSCCISSCYRPQCCQPSCC 185
                                                                                                                                                                                                                                                                                 92
                                                                                                   9
                                                                                                                                                77 PSCC-ISSCCRPSCCISSCC--KPSCC-RTTCCRPSCCISSCCRPSCCISSCCKPSC---
                                               24 CC-RPS----CC--QTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCLTTCCRTTCCR
                                                                                              6 CCGRPSIYSICCNIQETTFNTENOVWKCCTKKSPRKNCVARSGTPTLKKMSDPSKTNQCP
  47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ceccarelli A., McRobbie S.J., Jermyn K.A., Duffy K., Early A., Williams J.G.;
"Structural and functional characterization of a Dictyostelium gene encoding a DIF inducible, prestalk-enriched mRNA sequence.";
Nucleic Acids Res. 15:7463-7476(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRESTALK PROTEIN.
41 X 24 AA TANDEM REPEATS, CYS-RICH.
X-1.
X-2.
X-3.
A-1.
A-2.
B-1.
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MEDLINE=87257883; PubMed=3600646;

MEDLINE=87257883; PubMed=3600646;

MEDLINE=87257883; PubMed=3600646;

"Developmental regulation of DNase I-hypersensitive sites in Dictyostellum discoldenm.";

Mol. Cell. Biol. 7:1823-1829(1987).

"INDUCTION: BY THE PUTATIVE STATE, SPECIFIC MORPHOGEN DIF (DIFFERENTIATION INDUCTING FACTOR).

"INDUCTION: BY THE REPEATED SEQUENCES ARE HIGHLY HOMOLOGOUS TO A REPEAT OF THE PDD63 MRNA OF DICTYOSTELIUM DISCOIDEUM.
     63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida; Dictyostelium.
NCBI_TaxID•44689;
                                                                                                                                                                                                                                                                                                                                                                                                    DICDI SIGNE SIGNE PSTA DICDI SIGNE DI S
  Mismatches
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DictyDb; DD03006; ecmB.
InterPro; IPR001673; S_mold_repeat.
Pfam. PF00526; S_mold_repeat; 42.
ProDom; PD006869; S_mold_repeat; 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=AX2;
MEDLINE=88015608; Pubmed=3658700;
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61; Conservative
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Matches
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                   Drosophila melanogaster (Fruit fly).

Eukaryota: Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Peteryota; Neoptera; Endopterygota; Diptera: Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R TRANSFAC; T01688; -.

R FlyBase; FBgn0001978; stc.

R InterPro: IPR001374; R3H.

InterPro: IPR001841; Znf_Ling.

R InterPro: IPR001841; Znf_Ling.

R Pfam: PF01422; Zf-NF-X1; 8.

R Pfam: PF01424; R3H; 1.

R SMART; SM00184; RING; 1.

R SMART; SM0048; ZnF_NFX; 9.

R PROSITE; PS00139; ZnF_NFD_1; 1.

R PROSITE; PS00818; ZF_RING_1; FALSE_NEG.

R PROSITE; PS0089; ZF_RING_2; 1.

R TANSCTIPLION FG9118LING; DNA-binding; Nuclear protein; Repeat;
                                                                                                                         Stroumbakis N.D., Li Z., Tolias P.P.,
"A homolog of human transcription factor NF-X1 encoded by the Drosophila shuttle craft gene is required in the embryonic central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 X APPROXIMATE REPEATS, CYS-RICH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 210; DB 1; Length 1106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RING-TYPE
                                                                                                                                                                      Biol. 16:192-201(1996).
                                                                                                               MEDLINE-96104568; PubMed-8524296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U09306; AAB60255.1; -.
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Shuttle craft protein.
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464 50
517 55
575 61
634 67
723 76
834 87
109 1106 AA;
                                                                                         SEQUENCE FROM N.A.
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ZN_FING
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REPEAT
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15;

Gaps

22; Mismatches 120; Indels 122;

Pred. No. 1.6e-10;

22.48;

Conservative

Best Local Similarity Matches 76; Conserv

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                      577 DSCGOPLPCGHHKCKDSCHAGSCRPCKLSPEQ1TSCPCGKIPVPAGQRSSCLDP1PTCHG 636
                                                                                                                                             ------CKPSC-----C 100
                                                                                                                                                                               637 ICSRTLRCGKPAHPHO/GGSKCHLGOCPPCPKQTGVKCRCGHMDQMIKCRQL/CNRADDARC 696
                                                                                                                                                                                                                    RTTCCRPSCC1SSCCRPSCC--1SSCCRPSCCRTFCCRPSCC1SSCCRPSC--C1SSCCK 156
                                                                                                                                                                                                                                                      697 KRRCTKKRSCGKHKGNVECCIDIDIDHDCPLPCNRTLSCGKHKCDQPCHRGNCPPCYRSSFE 756
                                                                                                                                                                                                                                                                                                                PSCCQTTCCRPSCC1SSCYRDCC---QPSCCRPACC1SSC-----CH-----PSCCV 201
--- OTTUTE 36
                                                                       37 TTCCRPSCCISSCCRPSCCISSC--CKPSCCLTTCC-------RTTCCRP-SCCIS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Transcriptional repressor NF-X1 (Nuclear transcription factor, X hux-
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: BY INTERPERON GAMMA. SIMITLE CRAFT PROTEIN (STC) AND SIMILARITY: TO D.MELANGGSTER SHUTTLE CRAFT PROTEIN (STC) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=95053707; PubMed=7964459;
MEDLINE=95053707; Thanos D., Strominger J.L., Ono S.J.;
Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;
A novel cysteine-rich sequence-specific DNA-binding protein
interacts with the conserved X-box molif. of the human major
histocompatibility complex class II genes via a repeated Cys-His
                                                                                                                                                                                                                                                                                                                                                               202 SSCR-----CPFSCPTTCCRTTCFHPICCGSSCC 230
                                                                                                                                                                                                                                                                                                                                                                                                 810 FTTKLCHGNHDWRKTIPCSUPNFSCGMAGGKPLPCGGHKC 849
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                                                                                                                                             SCCR-------PSCCISSC-------
   CGSVCSD-QSCGOGLGQESCCRPSCC----
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Q12986;
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Gaps 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 LNCGRKLRCGLHRCEEPCHRGNC--QTCWQASFDELTCHCGASVIYPPVPCGTRPPECTQ 754
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R InterPro; IPR000967; Znf_NFX1.
R InterPro; IPR001965; Znf_PHD.
R InterPro; IPR001841; Znf_ring.
R Pfam; PF001422; zf_ring.
R Pfam; PF001422; zf_ring.
R SMART; SM00184; R134; 1.
SMART; SM00184; R105; 1.
R PROSITE; PS01018; ZF_PHD_1; UNKNOWN_1.
R PROSITE; PS01018; ZF_PHD_2; 1.
R PROSITE; PS0018; ZF_RING_1; FALSE_NEG.
R PROSITE; PS0018; ZF_RING_2; 1.
R PROSITE; PS0018; ZF_RING_1; PROSINGTE REPEATS, CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%; Score 198; DB 1; Length 1104; 21.9%; Pred. No. 1.5e-09; tive 18; Mismatches 118; Indels 150;
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Matches 80; Conservative
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647
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842
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424 46
480 51
541 58
606 64
695 73
806 84
843 87
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 11, 2003, 11:02:42; Search time 72 Seconds (without alignments) 425.662 Million cell updates/sec Run on:

1 MVSSCCGSVCSDQSCGQGLG......PTTCCRTTCFHPICCGSSCC 230 US-09-874-062-3 Title: Perfect score: Sequence:

Scoring table:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_101002:* Database :

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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/ SIDS2/godata/geneseq/geneseqp-emb1/AA1993.DAT:
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/ SIDS2/godata/geneseq/geneseqp-emb1/AA2001.DAT:
/ SIDS2/godata/geneseq/geneseqp-emb1/AA2001.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human four disulfi	Novel human diagno	Human protein SEQ	Human protein SEQ	Human hair keratin	Novel human diagno	Novel human diagno	Novel human diagno	Peptide #4761 enco	Peptide #4868 enco
	ID	AAE02058	ABG29368	AAM79986	AAM79002	ABB12277	ABG08337	ABG23698	ABG27981	ABB32110	ABB37362
	DB	22	22	22	22	22	22	22	22	22	22
	Length	230	206	301	250	120	256	351	267	231	231
æ	Query re Match Length DB I	100.0	82.1	51.7	51.1	40.4	37.2	37.2	35.3	34.6	34.6
	Score	1484	1218.5	167	758.5	299	552.5	552.5	523.5	513	513
:	Result No.		2	3	4	S	9	7	80	6	10

Protein #4647 enco	pra 11	one m	#	#	Peptide #4617 enco	Human peptide enco	Peptide #7027 enco	Protein #6265 enco	Human brain expres	Human bone marrow		Peptide #7105 enco	Human peptide enco	Peptide #6312 enco	Human brain expres	Human bone marrow	Peptide #6315 enco	Human peptide enco	Human protein SEQ		Novel human diagno	Human NOV3a protei	Novel human diagno	Human polypeptide	Human polypeptide	1-aminocyclopropan	Peptide #7583 enco	Protein #6565 enco	Human brain expres	Human bone marrow	Peptide #6429 enco	Peptide #7747 enco	Human peptide enco	Human epidermal pr
ABB22648	AAM38031	AAM70492	AAM18328	AAM30815	AAM05935	ABG40131	ABB39521	ABB24266	AAM60215	AAM72838	AAM19759	AAM33068	ABC42667	ABB38806	AAM59445	AAM72006	AAM32278	ABG41821	AAM79404	AAE18324	ABG26428	AAU91279	ABG19008	AAM41252	AAM39466	AAU07343	ABB40077	ABB24566	AAM60833	AAM73514	AAM19995	AAM33710	ABG43374	AAY44987
22	7 0	77	22	22	22	23	22	22	22	22	2.5	22	23	22	22	22	22	23	22	23	22	23	22	22	22	22	22	22	22	22	22	22	23	21
231	231	231	231	231	231	231	134	134	134	134	134	134	134	102	102	102	102	102	229	171	215	1329	398	222	167	1679		82				85		
4.			4.	34.6	34.6	34.6	31.4	31.4	31.4	31.4	31.4	31.4				•					٠		26.5								•			23.3
513	010	513	513	513	513	513		. 99	. 99	466.5	. 99	99	99	448	448	448	448	448	438.5	408.5	405	394.5	393	372	369.5	362.5	348.5	348.5	348.5	348.5		348.5		346.5
11	7 (FT :	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

AAE02058 standard; Protein; 230 AA (first entry) 10-AUG-2001 AAE02058; RESULT 1 AAE02058

Human four disulfide core domain (FDCD)-containing protein.

Human; four disulfide core domain; FDCD; immunosuppressive; cytostatic; antiarthritic; antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; dermacological; antiinflammatory; vulnerary antiarteriosclerotic; gene therapy; skin disorder; congenital disorder; mole; freckle; haemangioma; integumentary tumour; basal cell carcinoma; keratosis; melanoma; atherosclerosis; urticaria; photosensitivity; eczema; autoimmune disorder; lupus erythematosus; scleroderma; keloid; stria: erythema; petechia; purpura; xanthelasma; autoimmune discase; rheumatoid arthiitis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; neoplasm; angiogenesis; nervous system disorder; Alzhelmer's disease; infection; ocular disorder; corneal infection.

Homo sapiens.

WO200140249-A1.

29-NOV-2000; 2000WO-US32462.

99US-0168229 01-DEC-1999; ~

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCKPSCCQTTCCRPSCCISSCYRPQCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                  cerebral ischaemia, angiogenesis), nervous system disorders (e.g. Alzheimer's disease), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infection). The FDCD-containing proteins are used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary Lissues, to regenerate tissues and in chemotaxis. They are used in diagnosing a pathological condition or susceptibility to a pathological condition are used in alleviating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCC1SSCCRPSCC1SSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   symptoms associated with the disorders and in diagnostic immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). The FDCD sequences are also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                           containing protein from human. FDCD DNA and protein are used disorders e.g. moles, freckles and haemangiomas as well as congenital disorders e.g. moles, freckles and haemangiomas as well as integumentary tumours (keratosis, basal cell carcinoma, malignant melanoma), injuries and inflammation of the skin, atherosclerosis, urticaria, eczema, photosensitivity, autoimmune disorders (lupus erythematosus, soleroderma), keloids, striae, erythema, petechiae, purpura and xanthelasma. They are also used in the diagnosis and treatment of diseases and disorders of hair and epithelium, autoimmune diseases (e.g. rheumatoid arthritis), hyperpoliferative disorders (e.g. cardiac arrest), cerebrovascular disorders (e.g. cardiac arrest), cerebrovascular disorders (e.g.
                                                                                                            Four disulfide core domains (FDCD) containing polypeptide and its polynucleotide are used to prevent, treat or ameliorate a medical condition associated with FDCD e.g. skin disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1484; DB 22; Length 230; 100.0%; Pred. No. 2.9e-94; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCCTTTCFHPICCGSSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is four disulfide core domain (FDCD)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #29359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG29368 standard; Protein; 206 AA
                                                                                                                                                                      Claim 11; Page 230; 235pp; English
             (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 100.
Matches 230; Conservative
                                                                 WPI; 2001-356153/37.
N-PSDB; AAD06303.
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                                         Shi Y;
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                                        Ruben SM,
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polypeptide (II) sequences. (I) is useful as hybridisation prohes, polypeptide (II) sequences. (I) is useful as hybridisation prohes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markors and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KPSCCLTTTCCKTTCCRPSCC1SSCCRPSCC1SSCCKPSCCRTTCCRPSCC1SSCCRPSCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSSCCGSVCSDQS7XQQULGQESCCRPSCXQQPTCCRPTCCRPSCCISSCCRPSCX1SS7C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.1%; Score 1218.5; DB 22; Length 206: 84.3%; Pred. No. 3.2e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ 1D No 59727; 103pp; English.
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                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-USU8631.
                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                          11-OCT-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production of other cytokines in other cell populations. The polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 24 SSWDGS----RSLGRGLNHTSLNRSPPFTPDTWTHCCSPCCQPTCCRTTCCRTTCWRPTT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SCCISSCORPSCCISSCOK----PSCCLTTCCRTTCCRPSCCISSCORPSCCISSCOK 96
                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation.

Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ма
                                                                                                                            vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Cao Y,
Wang 2W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n P, Xu C
Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Asundi V, Zhou P, Wang J, Zhang J, Ren F, Che Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%; Score 767; DB 22;
46.9%; Pred. No. 2.2e-45;
iive 37; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Page 402; 6221pp; English.
AAM79986 standard; Protein; 301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            := := :: :: ::
                                                                                                                                                                                                                                                                                                                  200005-0560875.
200008-0598075.
200008-0654936.
200008-0654936.
200008-069325.
                                                                                    Human protein SEQ ID NO 3632.
                                                                                                                                                                                                                                                                         05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                      2000US-0496914
                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476283/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAK53119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                WO200157190-A2.
                                                                                                                                                                                                                                                                                                                  27-APR-2000; 2
20-JUN-2000; 2
19-JUL-2000; 2
                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2
15-SEP-2000; 2
20-OCT-2000; 3
30-NOV-2000; 2
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                      03-FEH-2000;
                                                       06-NOV-2001
                                                                                                                                                                                                                                             09-AUG-2001.
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                         AAM79986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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QQ
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammacomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
80 VTTCSSTPCCQPSCCVPSCCQPCCHPTCCQNTCCRTTCCQPT-CVASCCQPSCCSFPCCQ 138
                                                                    139 PTCCGSSCCCQTSCGSSCCQPICGSSCCQPCCHPTCYQTICFRTTCCQPTCCUPFCCRNF 198
                                                                                                      147 ---PSCC1SSCCKPSC-----CQTTCCRPSCC1SSCYRPQCCQPSCCRPACC1SSCC 195
                                  PSCCRTTCCRPSCC1SSCCRPSC---C1SSCCRPSC----C-RTTCCRPSCC1SSCCR-- 146
                                                                                                                                         SCQPTCCGSSCCQPCCHPTCCQTICKSTCCQPSCVTRCCSTP-CCQPTCGGSSCCSQTCN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; archritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Records for SEQ 1D NO 2110 (AAK52581), 2111 (AAK52582) and 3666
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<u>Z</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities,
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Ren F, Chen R, Wang
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Wang D, Wang J, Zhang J, Ren F, Che
                                                                                                                                                                          196 HPSCCVSSCRCPFSCPTTCCRTTCFHPICCGSSCC 230
                                                                                                                                                                                               Zhang J, Ren
F, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 4011-4012; 6221pp; Euglish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                  AAM79002 standard; Protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J, Zh
Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US - 0496914 .
2000US - 0568P7 .
2000US - 0598075 .
2000US - 0620325 .
2000US - 0654956 .
2000US - 063335 .
2000US - 0693325 .
                                                                                                                                                                                                                                                                                                                                                                                                           Human protein SEQ 1D NO 1664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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15-SEP-2000;
20-OCT-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                     AAM79002;
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RESULT 6
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                                                                               11;
                                                                                                                                                                                                                                            -----CQTTCCRPSCCISSCYRPQCCQPSCCRPACCISSCCHPSCCVSSCRCPFSCPT 212
                                                                                                                                                                                                                                                        165 PTCCQTICRSTCCQPSCVTRCCSTP-CCQPTCGGSSCCSQTCNESSYCLPCCR-PTCCQT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine; cell proliferation; cell differentiation; growth factor; ppoiesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                  SCCK----PSCCLTTCCRTTCCRPSCC1SSCCRPSCC1SSCCKPSCCRTTCCRPSCC1SS 113
                                                                                                                                                             CCRPSC---CISSCCKPSC----C-RTTCCRPSCCISSCCR-----PSCCISSCCKPSC- 159
                                                                                                                                                                                                                     CCQPICGSSCCQPCCHPTCYQTICFRTTCCQPTCCQPTCCRNTSCQPTCCGSSCCQPCCH 164
                                                                                                                 2 VSSCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRP----SCCISSCCRPSCCIS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
(AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoiesis regulation, tissue growth, immunomodulator, activin, inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins and DNA encoding sequences useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human hair keratin associated protein homologue, SEO ID NO: 2647.
                                                                              47;
                                                        Length 250;
                                                                               Indels
                                                       22;
                                                       51.1%; Score 758.5; DB 22; 47.3%; Pred. No. 7.3e-45; tive 37; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                       ABB12277 standard; peptide; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifungal; vulnerary; antiulcer
                                                                                                                                                                                                                                                                                                      223 TCYRTTCCRPSCCCSPCC 240
                                                                                                                                                                                                                                                                                         213 TCCRTTCFHPICCGSSCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT;
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27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-457740/49.
                                                                  122; Conserva
                                 250 AA;
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                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                              ABB12277;
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                                                       Query Match
                                                                     Local
                                                                              Matches
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potential uneapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis requilatory activity; tissue growth activity; immunomodulatory activity; activin. or inhibin-related activities; immunomodulatory activity activities or inhibin-related activities; chemotactic or chemokinetic activities; or inhibin-related activities; chemotactic or chemokinetic activities, proliferation or metastasis.

Thrombolytic activities, receptor or ligand activities; or may be involved in noncomeness, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleolides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., mysloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arthritis, vacual growth, Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wanned manding (e.g., of burns, include man ucers), while those accounts includes involved with the promote wanned manding elegance activities and utcers), while those accounts of the promote wanned manding elegance activities and utcers), while those accounts and utcers), while those accounts and utcers, while those accounts and utcers), while those accounts and utcers, when the accounts and utcers, while those accounts and utcers, while the accounts and utcers and utcers.
                                                                                                                                                                                                                                                                                                Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of polypeptides or polypeptides, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulatory activities may be used in the treatment of viral bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroeptide in cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KINSCCLIFFCCRFFFCCRPSCCLSSCCRPSCCTSSCCRPSCCRFFFCCRPSCCLISSCC_115
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treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
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Live 9; Mismatches 14; Indels 10
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                                                                                                                                                                                       Claim 20; Page 323; 1963pp; English
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                                                                        e.g. arthritis and cancer
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Matches 92; Conserv
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248 LSSGQKSSC 256
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23-AUG-2000;
                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                          polypeptide (II) sequences. (II) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in madical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCRPSCCRTTCCRPSCCISSCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPSCCISSCCKP-----SCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 CCISSCYRP-QCCQPSCCRPACCISSCCHPSCC-VSSCRCPFSCPTTCCRTTCFHPICCG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO at itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 VCSDQSCGQGLGQESC-----CRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISS--
                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 --IPSCCAPASTCQPSCCRPASCVSLLCRPTCSKLSSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.2%; Score 552.5; DB : 40.6%; Pred. No. 7.7e-31. iive 29; Mismatches 6
                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 38696; 103pp; English.
                                                                                                                                                                                                     Tang YT;
                                                                                                                                  31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                         30-MAR-2001; 2001WO-US08631
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Matches 101; Conservative
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                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AA;
                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                     W0200175067-A2.
                             Homo sapiens.
                                                                                                                                                                                                                                                                                                               biodiversity
                                                                               11-OCT-2001
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerates chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tays for identifying expressed genes. (I) is useful in gene therapy Lechniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, deterting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasoratics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and can amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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42.4%; Pred. No. 9.6e-31;
Live 28; Mismatches 59;
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                                                                                                                                                                                                                                       Novel human diagnostic protein #23689.
ABG23698 standard; Protein; 351 AA.
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2000US-0649167
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Best Local Similarity 42.48
Matches 97; Conservative
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267 AA;

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Sequence
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76 RPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKP-----S 128
              CCRTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRP-QCCQPSCCRP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                           188 ACCISSCCHPSCC-VSSCRCPFSCPTTCCRTTCFHPICCG-----SSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #27972.
                                                                                                                                                                                                          ABG27981 standard; Protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
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                                                                                                                                                                                                                                      ABG27981;
                                                    129
                                                                                                                                                                                RESULT 8
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142 SSCCRPSCCISSCCKPSCCQTTCC--RPSCCISSCYRPQCCQPSCCRPACCISSUCHPSC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                           96 K--PSCCRTTCCRPSCCISSCCRPSCCISSCCK------PSCCRTTCCRPSCCI 141
                                                                                                         ----OTTCCRTTCCRPS 43
                                                                                                                                                        SICSSACTDSWRVDDC-----PESCCEPCCCAPAPSLTLVCTPVSCVSSPCCQ--TACEPS 76
                                                                                                                                                                                                       44 CCIS---SCCRPSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCC----RPSCCISSCC 95
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #4761 encoded by breast cell single exon nucleic acid probe.
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                                                    73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 15078; 327pp + sequence listing; English.
       Length 267;
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                                                    Indels
                                                       . 89
                                                                                                         SCCGSVCSD----QSCGQGLGQESCCRPSCC-----
  Score 523.5; DB 7 Pred. No. 7.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 CVSSCRCPFSCPTTCCRTTCFHPICCG--SSC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 SRPAC-----YSLCSGQKSSC 267
                                                    32; Mismatches
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  35.3%;
36.4%;
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2000US-0608408.
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2000US-0234687
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Query Match
Best Local Similarity 36.4%
Matches 99; Conservative
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21-SEP-2000;
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04-OCT-2000;
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26-MAY-2000;
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analyzing gene expression in human fetal liver
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21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                            29 CCQTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCRPS
                                                                                                                                                                                                                                                                                                                 51 SCOPVVCEPSCCOPVCPTPTCSVTSSCOAVCCDPSPCEPSCSESSICOPATCVALVCEPV
                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #4868 encoded by human foetal liver single exon probe
                                                                                                                                                                                                34.6%; Score 513; DB 22; Length 231; 40.6%; Pred. No. 3.5e-28; tive 29; Mismatches 77; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                    -CVSSCRCPFSCPTTCCRTTCFHPICCGSSCC 230
                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB37362 standard; Peptide; 231
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2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                                                                       Conservative
                                                                                                                  probe of the invention.
                                                                                                                                                                                                          Local Similarity
nes 86; Conserv
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27-SEP-2000;
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                                                                                                                                                                           Sequence
                                                                                                                                                                                                 Query Match
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Matches
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89 CCISSCCKPSCCRTCCRPSCCISSCCRPSCCISSCCRPSCCRTCCRPSCCIS----S 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQCCQPSCCRPACCISSCCHPSC---- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein #4647 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                 measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 CCQTTCCRTTCCRPSCCISSCORPSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
Claim 27; SEQ ID NO 29997; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, gene expression, heart, microarray, vascular system;
cardiovascular disease, hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       34.6%; Score 513; DB 22; 40.6%; Pred. No. 3.5e-28;
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Penn SG,
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                                                                                                                     The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-BAB41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCQPVVCEPSCCQPVCPTPTCSVTSSCQAVCCDPSPCEPSCSESSICQPATCVALVCEPV 110
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                                                                                                                                                                                                                                                                                                                                            printed
                                                                                                                                                                                                                                      By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQCCQPSCCRPACCISSCCHPSC----
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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.6%; Score 513; DB 22; Length 231; 40.6%; Pred. No. 3.5e-28; Live 29; Mismatches 77; Indels 2
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2000US-0608408.
2000US-0632366.
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2000GB-0024263
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           231 AA;
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03-AUG-2000;
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04-OCT-2000;
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                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 CCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCRPSCCRTTCCRPSCCIS-----S 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                      Example 4; SEQ ID NO: 30156; 650pp + Sequence Listing; English.
                                                                                                                                                         present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                  Length 231;
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                                                                                                                                                                                                                                                                                                                                  34.6%; Score 513; DB 22; 40.6%; Pred. No. 3.5e-28;
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2000US-0236359.
2000GB-0024263.
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2000US-0207456
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2000US-0632366
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Matches 86; Conservative
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                                 MPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                   231 AA;
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27-SEP-2000;
04-OCT-2000;
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Claim 27; SEQ ID No 23154; 487pp; English.
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2000US-0632366.
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2000GB-0024263
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Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                        cervical cancer.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                           89 CCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCRTTCCRPSCCIS----S 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #4762 encoded by probe for measuring cervical gene expression.
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                                Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human bone marrow -
                                                                             Example 4; SEQ ID NO: 30798; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                  Length 231;
                                                                                                                                                                                                                                                  34.6%; Score 513; DB 22;
40.6%; Pred. No. 3.5e-28;
tive 29; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CVSSCRCPFSCPTTCCRTTCFHPICCGSSCC 230
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2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                 Similarity 40.6 86; Conservative
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WPI; 2001-488900/53
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30-JUN-2000;
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27-SEP-2000;
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The present invention relates to human single exon nucleic acid probes (SENP: see AA110068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human que expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCQPVVCEPSCCQPVCPTPTCSVTSSCQAVCCDPSPCEPSCSESSICQPATCVALV: EPV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
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analyzing gene expression in human cervical epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.6%; Score 513; DB 22; 40.6%; Pred. No. 3.5e-28;
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                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                             34.6%; Score 513; DB 22; Length 231;
40.6%; Pred. No. 3.5e-28;
Live 29; Mismatches 77; Indels 20; Gaps
               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 11, 2003, 11:04:04 Job time: 74 secs
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Best Local Similarity 40.6%;
Matches 86; Conservative
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                                                                                                         June 11, 2003, 11:02:46; Search time 27 Seconds (without alignments) 250.640 Million cell updates/sec
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Sequence 13,
Sequence 13,
Sequence 11,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  version 5.1.6
- 2003 Compugen Ltd.
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US-08-977-767-3

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US-09-627-6508-5

US-09-436-063C-5

US-09-548-372D-13

US-09-627-6508-11

US-09-627-6508-11

US-09-627-6508-1

US-09-637-6508-7

US-09-436-063C-1

US-09-627-6508-7

US-09-627-6508-7

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US-09-637-6508-7

US-09-436-063C-3

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US-08-828-544-5

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Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
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                                                                                                                                                                                                                               Sequence 16,
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Sequence 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCOMMATION:
APPLICANT: Bard, Jonathan A.
TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDIRESS:
ADDRESSEE: Cooper & Dunham Lup
STREET: 1185 Avenue of The Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 412; DB 4; Length 1417;
; Pred. No. 8.8e-24;
13; Mismatches 97; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CCGSVCSDQSCGQGL-----GQESCCRPSCCQ-----TTCCRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                         US-08-185-11684-2
US-08-185-432-16
US-08-083-590A-19
US-08-532-384-19
US-08-899-232-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/900,230
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
ATTORNEY/GRATION: 435
ATTORNEY/GRATION: NAME: White, John P. REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
                                            US-09-467-997-1
US-08-527-044-2
US-08-527-044-2
US-09-013-780-2
US-08-68-648-2
US-08-429-998-2
US-08-431-333-2
PCT-US91-0231-2
PCT-US95-11684-4
                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08900230 Patent No. 6329197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1417 amino acids
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Best Local Similarity 33.1°
Matches 92; Conservative
COMPUTER READABLE FORM:
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STRANDEDNESS: sir
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RESULT 4
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                   1066 ---CACTTCCGCGCGCGC-TTCCGCCGCCTGTGGCCGTGC--GGCC--GCCGACGCCGCC 1117
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                                                                     -----CRPSCCISSC-C 145
                                                                                                                                            RPSCCISSCCKPSC---CQTTCC-----RPSCCISSCYRPQCCQPSCCRP-ACC-IS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 SSCCKPSC------CQTTCCRPSCCISSCYRPQCCQPSCCRPACCISSC---- 194
-CCRPSCCISSCCR--PSCCISSCCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SSCCGSV------CSDQSC----GQGLGQESCCR------PSCCQTTC--CRTTCCR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 PSCCISSCCRPSCCISSCCKPSCC---LTTCCRTTCCKPS-----CCISSCCRPSCCI 91
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: MOCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00849
CURRENT APPLICATION NUMBER: US/09/738,884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1195 GACATGCTGGTGACACAGGCGCTGGACTCCCCAAATC----CCGAGGAGCTGCC 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 -- CHPSC-----SSCRCPFSCPTTCC--RTTCFHPICCG-----SSCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.8%; Score 412; DB 4; Length 2211; 29.9%; Pred. No. 1.2e-23; Live 19; Mismatches 99; Indels 8
                                                                                                                                                                                                                                      193 SCCHPSCCVSSCRCPFSCPTTCCRTTCFHPICCGSSCC 230
                                                                   96 KPSCCRTTCCRPSCCISSCCRPSCCRTTC-
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Patent No. 5972684
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Yue, Henry
APPLICANT: Creenwald, Sara
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09738884 Patent No. 6391606 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human
US-09-738-884-1
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Matches 8
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974 CGGAGACTGTTACCFGGATCCTCATTGACAGGGCCCTCAATATCACCTCCCTCCAGCFGC 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CCG----SVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCI-SSCCRP----SCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1345;
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Live 22; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26:4%; Score 391.5; DB 2;
                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,767
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NIMBER: PF-0423 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 37, Application US/U8630915A
; Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, NO. 6309820h
APPLICANT: KAY, BIJAN K.
APPLICANT: FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                              COMPUTER FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1345 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                 COMPUTER: 1BM Com
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: General 1532042
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                                                                                                                     USA
                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                      94304
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                                                                                                                     COUNTRY:
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us-09-874-062-3.rai

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1566 TGTATCAGAC 1575
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LENGTH: 1917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PSCISSCCRPSCLISSCCKPSCQ--TTCCRPSCCI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 PSCCISS-----CCKPSCCLTT-----CCR-TTCCRPSCCISSCCRPSCC-- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CCGSVCSDQSCGQGLGQESCCR------PSC--CQTTCCRTTCCRPSCCISSCCR 51
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 ACGGATAACTGGGATGCATGGCCAGCCCACCTCTCTCACCGTTCCAAGTGCC-GGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 SSCYRPQCCQP--SCCRPACCISSCCHPSCCVSSCRCPFSCP----TTCCRTTCFHPICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 GTTAAGGCAGGGTCC--GCCTTTAC--TCCAGGCCACGGCCACGGCTCC--TC--CCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.5%; Score 378; DB 4; Length 1400; 28.8%; Pred. No. 2.9e-21; Live 23; Mismatches 95; Indels 100
                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09627650B Patent No. 6406872 GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                         18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1400 amino acids
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.59
Best Local Similarity 28.89
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                     NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 GS-SCC 230
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GTCTCC 654
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                                                                                                                                                             New York
                                                                                                                                                                                               10036-2711
                                                                                                                                           New York
                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1281 CCGTCGCATACATCACCAAACGGATGAAGCTTGTCCGAGCCAGAAAAGAATCTCGAATGT 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 -----RTTCCRPSCCISSCCRPSCCISSCCRPSCCRTT---CCRPSCCISSCCRPSC--- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 CCG------SVCSD--QSCCQGLGQESCCRPSCCQTTCC------RIPGCRPSCC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 PSCC----RPACCLISSCCHPSCCVS-------SCRCPFSCHTFC--CRFTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Brik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-09
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APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92; Indels 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 ---CISSCOKPSCCQFTCCRPS-----CCISSCYRPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.6%; Score 365; DB 4; Best Local Similarity 27.1%; Pred. No. 3.4e-20; Matches 84; Conservative 34; Mismatches 92
                                                                          FILE REFERENCE: 21101.000903
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 2000-07-28
FRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SECTION OF SEQ ID NOS: 55
LENGTH: 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09436063C Patent No. 6407210 GENERAL INFORMATION:
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US-09-436-063C-5
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Caenorhabditis elegans US-09-627-6508-5
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SOFTWARE: Patentin Ver. 2.1
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Matches 84; Conservative
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TITLE OF INVENTION: ALZHEIMEK'S DISEASE SECRETASE, APP SUBSTRATES THEKEFOR AND USE TITLE OF INVENTION: THEREOF FILE REFERENCE: 29915/6280H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 CACATGAATGTGGAAATGGGAAGTGGGATTCAGATCCATCAGGGACGAAAAGTTGATT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 GATACCAAGGAAGGATCCTGCAGTATTGCCAAGAAGTCTACCCTGAACTGGAGATGAGCTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 GCAGTGCAAGACCCATCCCCAGTTTGTGAFTCCCTACCGCT-GCTTAGTTGGTGGTGGTTTG 367
3 SSCCGSVCSDQSCCQQCLCQESCCRPSCC --- QTTCCR--TTCCRPSCC1SSCCRPSCC1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 SCCKPSCCLPPCC------KPPCCRPSCCIS----SCCKPSCCISSCC--
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Patent No. 6406872

GENERAL INFORMATION:

A APPLICANT: Bamber, Bruce

A APPLICANT: Jorgenseh, Erik

TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and

TITLE OF INVENTION: Methods Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.8%; Score 338.5; DB 4; 24.5%; Pred. No. 3.3e-18; ive 25; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCIYUS99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 -----CCRTTCFHPICCGSSCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 TAAGTGATGCCTTTC---TGGTTGC 389
                                                                                       214 ------CCRTTCFHPICCGSSCC 230
                                                                                                                                                                                                           Sequence 13, Application US/U9548367D Patent No. 6440698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.8%
Best Local Similarity 24.5%
Matches 80; Conservative
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-627-650B-11
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TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT APPLICATION NUMBER: US/09/548,332D
CURRENT APPLICATION NUMBER: US/09/54,493
PRIOR APPLICATION NUMBER: US/09/23
PRIOR PILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1998-09-24
SOFTWARE: PARENTIN NUMBER: US/09/24
SOFTWARE: PARENTIN VERSION 3.1
SOFTWARE: PARENTIN VERSION 3.1
                                                                                                           :|| | ::|| ::|| :|| :|| 341 TGACC--CCTTTACCACACATCTTGAGTCTCTTCC--TCCAAAAACGTACTCTTATCCGTTCCC 1396
                                                                                                                                                                                                1449 CGTCCAACCTGTACATTCCGGAGTCGCAGCGCACGATTTTCTCAAATGAGGATGCAG 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 -KPSCCR-----TTCC-----RPSCCISSC---CRPSCCISSCCKP-----SCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GATACCAAGGAAGGCATCCTGCAGTATTGCCAAGAAGTCTACCCTGAACTGCAGATCACC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 RTT------CCRPSCCISSCCRPSCCISSCCKPSCCQ-TTCCRPSC-----CIS 172
                                                                                                                                                                                                                                                                                                                                            182 PSCC---RPACCISSCCHPSCCVS------SCRCPFSCPTTC--CRTTC 219
                                                                                  46 ISSCCRPSCCISSCCKPSCCLT---TCCRTTCCRPSCCISSCCRPSC-CISSCCKPSC- 100
                                                                                                                                                                     101 ----RTTCCRPSCCISSCCRPSCCISSCCRPSCCRTT---CCRPSCCISSCCRPSC--- 149
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CCG----SVCSD--QSCGQGLGQESCCRPSCCQTTCC---
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; Patent No. 6420534
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APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
TITLE OF INVENTION: Methods Related Thereto
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION UNMBER: 60/107727
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                                                                                                                                                                                                                                                                                       DB 4; Length 1128
                                                                                                                                                                                                                                                                                   Query Match 21.3%; Score 316.5; DB 4; Length Best Local Similarity 25.1%; Pred. No. 9.2e-17; Matches 76; Conservative 27; Mismatches 111; Indels
FILE REFERENCE: 21101.000903
CURKENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 2000-07-28
PRIOR PRICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
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Patent No. 6407210
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ORGANISM: Caenorhabditis elegans
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ORGANISM: Caenorhabditis elegans
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NUMBER OF SEQ ID NOS: 18
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Matches 76; Conserv
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1009 TGC 1011
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952 TTCATTAATCHCAATCC--AACTTCCTCA-TCATTTTCCATTTCGAATATCTCHPPPPT 1008
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60 CKPSCCLTTCCWTTCCRPSCCISSC-CRPSCCISS-------CCKPSCC---KPT 103
                                                                                                            ----PSCCISSC-CRPSCCISSCCKPSCCRTTCCRPSCCISSCCRP 147
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APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Mentadde Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U3
CURRENT APPLICATION NUMBER: US/09/627,650B
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
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Patent No. 6406872
GENERAL INFORMATION:
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SEQ ID NO 1
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SEQ ID NO 7
ORGANISM:
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APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 2110.000903
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 2000-07-28
                                                                                          GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
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                                                                                                                                                                                    FILE REFERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107727
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
SOFWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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; Patent No. 6406872
                                                     Sequence 1, Application US/09436063C Patent No. 6407210
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Caenorhabditis elegans
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SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 2508
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2106 TCCG-CCTTGCCGAATGCAACGCGGGCTCCAACCTCGATCATCGCCGTCATCATG 2164
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APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptur's and
TITLE OF INVENTION: Membods Related Thereto
FILE REFERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: U5/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107727
NUMBER OF SEQ ID NUCS: 18
SOFTWARE: PatentIn Ver. 2.1
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Live 27; Mismatches 111; Indels
                                                                                                                       Indels
                                                                   Query Match 21.3%; Score 316.5; DB 4; Best Local Similarity 25.1%; Pred. No. 1.6e-16; Matches 76; Conservative 27; Mismatches 111;
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; Patent No. 6407210
; GENERAL INFORMATION:
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ORGANISM: Caenorhabditis elegans
Caenorhabditis elegans
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Best Local Similarity 25.1%
Matches 76; Conservative
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US-09-436-063C-7
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                          US-09-627-650B-7
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2284 GCGICTGCCGTATATTAGTGAACACGAGGTGACCGTTGCGATGC-----TCCAGACC 2336
                                                                      2337 TICATTAATCTCAATCC--AACTTCCTCA-TCATTTTCCATTTCGAATATCTCTTTTTCT 2393
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                                             186 RPAC-----CISSCCHPSCCVSSCRCPFSC--PTTCCRT------TCFHPICCG 226
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APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 2101.0009013
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR PLIING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 3.
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Best Local Similarity 25.1%; Pred. No. 1.6e-16;
Matches 76; Conservative 27; Mismatches 111; Indels 89; Gaps
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Job time : 29 secs
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; ORGANISM: Caenorhabditis elegans
US-09-627-650B-3
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US-09-627-650B-3
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064507	O9BYR4	028576	Q9BYQ7	Q9BYQ4	Q28707	070148	090225	Q9BYQ0	09BYQ3	09BY02	Q9BYQ9	Q9BYP9	Q9BYU7 .	007628	007627	Q9BYS1	Q9BYS2	029619	014564	1 090527	l Q9D644	092287	Q9BYQ1	017982	1 090718	029620
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17	0 0	20	21	22	23	24	25	56	27	58	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44

ALIGNMENTS

Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S., Anadawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Akuehl P., Lewis S., Matsuo Y., Nikaido I., Resoliva H., Washio T., Saxuki R., Comita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whitmay H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Washii Y., Kawaji H., Kohtsuki S., 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1110054P19R1K protein.
1110054P19R1K.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi: Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musinae: "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
BMBL; AK004258; BAB23238.1; -. HSSP: O46655; ICJH. 195 AA PRT; SEQUENCE FROM N.A. STRAIN-CS7BL/6J; TISSUE"EMBRYO; MEDLINE-21085660; PubMed=11217851; PRELIMINARY; Hayashizaki Y.; 9500x9 RESULT 1 9500x9

June 11, 2003, 11:02:46; Search time 78 Seconds (without alignments) 607.575 Million cell updates/se 1 MVSSCCGSVCSDQSCGQGLG......PTTCCRTTCFHPICCGSSCC 230 5.1.6 Compugen Ltd. Total number of hits satisfying chosen parameters: 671580 seqs, 206047115 residues GenCore version Copyright (c) 1993 - 2003 OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv length: 0 length: 2000000000 US-09-874-062-3 1484 Title: Perfect score: Sequence: Scoring table: Minimum DB seq Maximum DB seq Run on:

sp_archea:* sp_bacteria:* SPTREMBL_21:* Database

summaries

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:* sp_unclassified:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_plant:*
sp_rodent:* sp_virus:* sp_phage: * sb_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

Query Match Length DB Score

Q9byr0 homo sapien Q9byq6 homo sapien Q9byq6 homo sapien Q9byq8 homo sapien Q9byq5 homo sapien Q91w93 mus musculu Q9dyp3 mus musculu Q9byr2 homo sapien Q9byr3 homo sapien Q9d122 mus musculu Q9d3h7 mus musculu Q64526 mus musculu Q62220 mus musculu O9d141 mus musculu Q9d0x9 mus musculu Description 0900x9 099xR0 098066 099x06 099x08 091x05 091x83 090732 090732 090732 090732 50.1 49.7 47.8 46.7 804.5 800.5 764.5 744 866.5 858.5 808.5 806 Result

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121
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                                                                                                             RTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQC----CQPSCCR 186
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 61
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                                     RPSCCISSCCRPS----CCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCC
                                                        17 QGLGQESCCRESCCQFFCCRFFCCRESCCISSCCRPSCCISSCCK-----PSCCLT
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to RIKEN cDNA 1110054P19 gene.
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01-JUN-2001 (TrEMBLrel, 17, Last seq
01-MAR-2002 (TrEMBLrel, 20, Last anno
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Matches 133; Conservative
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                                                                                                             131
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                                                                                                                                                                                                                                                                                                                                                                                                                        KPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRPQC- 179
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                                   Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.; "Characterization of a cluster of human high/ultrahigh keratin associated proteins on chromosome 17q12-21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVSSCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCC
                                                                                                                                                                                                                                                                                                                                                                       21 QESCCRPSCCQTTCCRTTCCRPSCCISSCCRPSCCISSCC----KPSCCLTTCCRTTCC
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukuryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.4%; Score 866.5; DB 4; Length 191; 66.7%; Pred. No. 6.5e-97; ive 18; Mismatches 25; Indels 23.
                                                                                                                                                                                                                                                                            Length 195;
                                                                                                                                                                                                                                                                                                                31; Indels
                                                                                     Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases. EMEL: AJ406944; CAC27583.1; -...
InterPro; IPR001494; Keratin_B2.
InterPro; IPR001368; TNFR_C6.
InterPro; IPR001007; VWF_C.
Priam; PF01500; Keratin_B2; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PKOSITE; PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20572 MW; 3B1C0044ADB340C6 CRC64;
                                                                                                                                                                                                                                      20799 MW; 59F85D74C3D5307E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Last sequence update)
, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 898; DB 4; 1
Pred. No. 1.1e-100;
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                                                                                                                                                                                                                                                                                                              23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keratin associated protein 4.9 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 GVSCHTTCYRPTCVISSCPRPLCCASSC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00652; TWFR_NGFR_1; UNKNOWN_1
PROSITE; PS01208; VWFC; UNKNOWN_1
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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InterPro; IPR001368; TNFR_c6.
InterPro; IPR001007; VWF_C.
Pfam; PF01500; Keratin_B2; 1.
                                                                                                                                                                                                                                                                        60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.79
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                      195 AA;
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                                                                                                                                                                                                                                                                                             3est Local Similarity
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 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      SEQUENCE
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Hayashizaki Y.;
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EMBL: AJ406936; CAC27575.1; -...
InterPro: IPR001249; Reratin_B2.
InterPro: IPR001368; TNFR_C6.
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MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.9%; Score 800.5; DB 4; Length 166; 65.4%; Pred. No. 5.1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                       166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
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                                                                                                                       PRT;
                                                                                                                                                                                                                        Keratin associated protein 4.4.
17,
21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121; Conservative
                                                                                                                       PRELIMINARY;
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2310037K05RIK.
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Best Local Similarity
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                                                                                                                                            Q9BYR3;
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                                                                                                                       O9BYR3
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09D732
                                                                           RESULT 10
Q9BYR3
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A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawnt T., Relischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Schimal L., Stauki R., Tomita M., Magner L., Washio T., Rashi F., Sazuki R., Tomita M., Wagner L., Washio T., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Burnstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Anonoser, M. Gustincich S., Hill D., Hofmann M., Hame D.A., Kamiga M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whitcher C., Wilming L., Myshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCCRPSCC 120
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Mammalia; Eutheria; Rodenlia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Mature 409:685-690(2001).
BMBL: AKO09665: BAB26426.1; -.
HSSP: O46655: ICJH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.5%; Score 764.5; DB 11; Length Best Local Similarity 63.8%; Pred. No. 1.1e-84; Matches 118; Conservative 18; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ul-JUN-2002 (TrEMHLrel. 17, Last Sequence update)
Ul-JUN-2002 (TrEMHLrel. 21, Last annotation update)
clone:Illo030N11, full insert sequence.
Mus musculus (Mouse).
Eukaryota: Matri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17568 MW; A99E4AB35B30D386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1923694; 2310037K05kik.
InterPro; 1PR000561; EGF-1ike.
InterPro; 1PR001494; Keratin_B2.
InterPro; 1PR001007; VWF.C.
Pfam; PF01500; Keratin_B2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 ATPCC 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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SCCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCRPSCCRTTCCRPSCCISSCCRP 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCCQPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCCRTTCFHPIC------CGS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCCOP-CCOTTCCRT-------CFOPCCVSSCCRTPCCQPCCVSSCCQP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSSCCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSC---CISSCCRPSCCIS 57
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
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MEDLINE=89140394; PubMed=2465353;
MCNab A.R., Wood L., Theriault N., Gierman T., Vogeli G.;
"An ultra-high sulfur keratin gene is expressed specifically during hair growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
YCHI_TaxID=10090;
                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
Nature 409:685-690(2001).
Inter 409:685-690(2001).
InterPro: IPR001494; Keratin_B2.
InterPro: IPR001109; Thionin.
InterPro: IPR001109; Thionin.
InterPro: IPR001109; TWF_C6.
InterPro: IPR001109; TWF_C6.
InterPro: IPR001109; TWF_C6.
PROSITE: PS00271; THIONIN; UNKNOWN_1.
PROSITE: PS00052; TWF_C9.
PROSITE: PS00052; TWF_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.8%; Score 709; DB 11; Length 191; 49.4%; Pred. No. 5.9e-78;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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InterPro: IPR001010; Thionin.
InterPro: IPR001010; TNFR_C6.
InterPro: IPR001007; VWF.C.
Pfam; PF01500; Keratin_B2; 1.
PROSITE; PS00621; THRONIN: 1.
PROSITE; PS00652; TWFR_NFR_L; UNKNOWN_I.
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-!- SIMILARITY: TO THE PLANT THIONIN FAMILY
EMBL: M27685; AAA81560.1; --
MGD; MGI:1309997; Krtap9-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Mismatches
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Matches 120; Conservative
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| SCC 186
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58 SCCKPSCCLTTCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCRTTCCRPSCCISSCHWP 117
                                                                                                                                                                                                118 SCCISSCCKPSCCRTTCCRPSCCISSCCRPSCCISSCCKPSCCQTTCCRPSCCISSCYRP 177
                                                                                                                                                                                                                                                       178 QCCQPSCCRPACCISSCCHPSCCVSSCRCPFSCPTTCCRTTCFHPIC------CGS 227
                                                                                                  1 MVSSCGSVCSDQSCGQGLGQESCCRPSCCQTTCCRTTCCRPSC---CISSCGRPSCTS
                           DB 11; Length 186;
                                                      Indels
19658 MW; 61D6BFDAB72CFEB4 CRC64;
                    47.3%; Score 701.5; DB 11;
49.0%; Pred. No. 4.6e-77;
Live 20; Mismatches 29;
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ne : 80 secs
                                       Best Local Similarity 49.0%;
Matches 119; Conservative
 186 AA;
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SEQUENCE
                             Query Match
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1063\0 CARTATACATAAATCTTCAAATGGTATCCTTCTAGATGTTTCTTCCTAATGTTTTCTGTG 106419

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(961 CANTATACATAAATCTTCAAATGGTATCCTTCTAGATGTTTCTTCCTAATGTTTTCTGTG 1020

146300 TTGAATCTGAATTTACAGTCAAATTCCACATCACATGTTTTAGAACTCTTTATTCTAATT 106359

/ Organism="Homo sa / Ab_xref="taxon:99	T 88	Duery Match Best Local Similarity Matches 1002; Conset Ouery Match Best Local Similarity Duery Match Db 105475 CTGGGAACC Oy 121 TGCTGCTGT Oy 241 TGCTGCTGT Oy 241 TGCTGCTGT Oy 361 TGCTGCAGG Oy 361 TGCTGCAGG Oy 421 TGCTGCATT Db 105820 TGCTGTATC Oy 481 TGCTGTATC Oy 481 TGCTGTATC Oy 661 TGCTGTATC Oy 661 TGCTGTATC Oy 661 TGCTGTATC Oy 661 TGCTGCATT Ob 10590 TGCTGTATC Oy 661 TGCTGCATT Oy 781 TGCTGCTATC Oy 781 TGCTGCTATC Oy 781 TGCTGCTATT Oy 781 GCACAGGT Oy 781 TGATGATTT Oy 841 GACTGATTT Oy 841 GACTGATTT Oy 781 TGATGATTT OY 781 TGATGATT OY 781 TGATGAT OY 781 TGATGAT OY 781 TGATGAT OY 781 TGATGAT OY	rganism-"Homo sapiens" b_xref="taxon:9606" hromosome="3": lone="Rp11-595122" 64859 c 63333 g 108900 t 3154 others	60 GD	AACCAGAACCTCCACCCTCTGACGCCATGGTCACTCTGCTGTGGCTCT 60	GTCTGCTCTGACCAGGCTGTGAGGTCTCGGCCAGAGAGCTGCTGCCGCCCAGC 120	180	HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCTTCC GCTGTATCTCCAGCTGCTGCAACCCAGCTGCTGCCTGACCACC 240	VGCCGCCCCAGCTGCTGCATTCCAGTTGCTGCAGGCCTTCC 300.	ACCACCAGCAGAACCACAGCAGAAGAACACACAGCAGCAG		TGCTGCATTTCCAGTTGCTGCAGACCTTCCTGCTGTATCTCCAGCTGCTGCAACCCAGC 420			CTGCAGGACCACCTGCTGCCGCCCCCAACTGCTAGTTGCTGCAGGCCTTCC 105879	TGCTGTATCTCTAGCTGCTGCAAACCCAGAGCGCAGCCACCTGCTGCCGCCCCAGC 540 	TGCTGTATCTCCAGCTACAGGCCCCAGTGCCGGCCTCCTGCTGCCGCCCGGCT 600	TGCTGCATITCTAGTTGCTGTCATCCCAGCTGCTGTTGCCGCTGCCGTTTC 660	recrecarriciaerrecrerecrecrecrererererecrecrecrecrererer 106059	AGCTGCCCGACCTGCTGTAGAACACCTGCTTCCAC&CCATCTGCGGCACTTCT 720 	TGCTGCTGAGTGAAGCTGCTCTGGATTTGTGCACCTTCTTGCACCTTCAGTTCAG 780	TGCTGCTGAAGCTGCTCTGGATTGTGCACCTTCTTGCTGTCAACCTTCAGTTCAG 106179	GCACAGAGTATCTATTCAGAGAACATGTGGACTTCCTGATGTCGTOAAAACAGAGGCATG 840 	006	GACTGATTTGGAAAATATTTATTAGTATGTATTCTCTTTTATAGAAGTTTATATTACTA 106299	TIGAATCTGAATTTACAGICAAATTCCACATCACATGTTTAGAATTCTTTATACTAATT 960
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DD 1064 DD 1064 QY 10 DD 1064 ACCOSION VERSION VAUTHORS AUTHORS AUTHORS AUTHORS AUTHORS COMMENT	1021 GTATCAATTTTCATGGGAATTGTTTGATGTTTCCTCAATAAAACTTCATAGTGTTCAAAA 1080 106420 GTATCAATTTTCATGTGGAATTGTTTGATGTTCCTCAATAAAACTTCATAGTGTTCAAAA 106479 1081 GCAAAAAAA 1090	ACO06070 ACO06070 ACO06070 ACO06070 ACO06070 ACO06070 HTG. HTG. HTG. BOME Sapiens. Homo sapiens. Hom	1 (bases I to 161987) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.206_C_20 Unpublished 2 (bases I to 161987) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cocke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Bonelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geralgery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kan, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., Mychalecky, J., Waldrim, J., Molla, M., Morrow, J., Mychalecky, J., Waldrim, J., Nuloff, M., O'Conoor, T., Mychalecky, J., Waldrim, J., Nuloff, M., O'Conoor, T.,	O'Donnell, F., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliav, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M. Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M. Whitehead Institute/MIT Center for Genome Submitted (26-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 161987) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArtellano, K., Depayter, E., Devon, K., Depayte, R., Devon, K., Depayter, E., Devon, K., Departe, R., Devon, R., Danelan, I., Ferreira P., Firkhuch W., Forrest F.	Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Uerran, L., Horton, L., Howland, J.C., Jones,C., Kann,L., Karatas,A., Lehoczky,J., Macdonald,P., Marquis,N., McGurk,A., McKernan,K., Meldim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Rilay,R., Roberts,D., Roy,A., Severy,B., Stange-Thoman,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Myman,D., Ye,W.J. and 2ody,M. Direct Submission L. Submitted (17 DEC 1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 17, 1998 this sequence version replaced 91:4006836. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Only the last 161987 base pairs of this clone are being submitted.

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79.6%; Score 876.8; DB 9; Length 161987;
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complement(30929, 314000)
rpt family
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:645. .337<
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omplement/?family="Lima9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(37178. .37548)
/rpt_family="MLT1B"
complement(37860. .38117)
                                                                                                                                                                               rpt_family="Alusx"
9095, .19504
                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="LiPA2"
umplement'()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nplement(28515. 28581)
pt_family="purine-rich"
nplement(28582. 28674)
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1091.
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/rpt_family="LlM3e"
36529. .36637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="polypurine",
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38432, .38695
                                                                      complement(16870. .16897)
/rpt_family="(CAAAAA)n"
complement(17088. .17221)
                                                                                                               /rpt_family="Alusg/x"
complement[17989. .18273)
/rpt_family="Alusx"
18409. .18438
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omplement(28116. .28209)
rpt_family="MLTIC"
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180, _203=
                16482. .16555
/rpt_family~"(GAAA)n"
16556. .16727
/rpt_family="AluSq"
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/rpt_family="AT_rich"
complement(33997. .34)
                                                                                                                                                                      rpt_family "AT_rich"
omplement(18439. .18
                                                                                                                                                                                                                                                                                                                                                                      rpt_family="AT_rich"
omplement(25352. .25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="LTR16C"
                                                                                                                                                                                                                                                                                     .y-"AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pt_family="LTR16C"
1760. .33915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pt_family="LTR16C"
3355_ .29510
                                                                                                                                                                                                                     rpt_family="MER31B"
1277
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omplement(32754. ..
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24184. 24291
/rpt_family="MIR"
25327. 25351
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3929. .33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pt_family-"MIR"
524. .29569
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3843. .23
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     Irren, B., Linton, L., Nusbaum, C. and Lander, E. Mon sapiens, clone RP11-585G19
                                 HTG; HTGS_PHASE1; HTGS_DRAFT
 AC025904
AC025904.2 GI:7382590
                                                                                                                     (bases 1 to 174032)
                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                               971 AAATCTTCAAATGGTATCCTTCTAGATGTTTCTTCCTAATGTTTTCTGTGGTATCAATTT 1030
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                                                 131 CCACCTGCTGCAGGACCACCTGCTGCCGCCCCAGCTGCTGCATTTCCAGTTGCTGCAGGC 190
                                                                                                                                                                                         CCACCTGCTGCCGCCCCAGCTGCATTTCCAGTTGCTGCAGGCCTTCCTGCTGTATCT 310
                                                                                                                                                                                                                                                                                                                               CCAGTTGCTGCAGGCCTTCCTGCTGTATCTCCAGCTGCTGCAAACCCAGCTGCTGCTGCAGGA 430
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94.6%; Pred. No. 2.4e-142; ive 0; Mismatches 52;
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908; Conservative
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Best Local
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AC239U4 174032 bp DNA linear HTG 26-MAY-2000 HOMD capiens clone RPl1-585G19, WORKING DRAFT SEQUENCE, 17 unordered pieces.

LOCUS AC025904 🗷 RESULT

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Andergon, S., Baldwin, J., Barna, M., Bastien, V., Beda, F., Baldwin, J., Barna, M., Bastien, V., Beda, F., Bornan, R., Batten, V., Beda, F., Baldwin, J., Barna, M., Bastien, V., Beda, F., Boguslavkiy, L., Boukhajler, B., Brown, A., Burkett, G., Campopiano, R., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D., Galdgan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L., Karatas, A., Klein, J., Larkque, K., Landers, T., Lehoczky, J., Klein, J., Larkque, K., Landers, T., Lehoczky, J., McCarthy, M., McWan, P., McCurthy, M., McWan, P., McCurth, A., McKernan, K., Menquis, N., McCarthy, M., McWan, P., McCurk, A., McKernan, C., Menquis, N., McCarthy, M., McWan, P., McCurk, A., McKernan, C., Menquis, N., McInd, J., Lankque, C., Liu, G., Locke, K., Macdonald, P., Marquis, V., McCarth, M., Miranda, C., Menquis, N., McInd, J., Mendy, T., Moylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Plsani, C., Pollara, W., Raymon, C., Riley, R., Rogov, P., Rothman, D., Plsani, C., Pollara, W., Raymon, C., Subramanian, A., Talamás, J., Tesfaye, S., Theodore, W., Milson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Travers, M., Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kesearch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             currently
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Sequencing vector: M1: M7815: 100% of reads Sequencing vector: M3: M7815: 100% of reads Chemistry: Dye-terminator B19 Dye: 100% of reads Assembly program: Phrap; version 0.940731
Consensus quality: 158771 bases at least 040
Consensus quality: 158771 bases at least 030
Consensus quality: 170560 bases at least 020
Insert size: 170000: agarose-fp
Insert size: 172432: sum-of-contigs
Quality coverage: 3.9 in 020 bases; sum-of contigs
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions&genome.wi.mit.edu
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2589 2688: gap of 100 bp
2689 6465: contig of 3777 bp in length
6566 8846: contig of 3777 bp in length
6566
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 11, 2003, 11:02:46; Search time 18 Seconds (Without alignments) 1228.384 Million cell updates/sec

US-09-874-062-3 1484 1 WYSSCGSVCSDQSCGQGLG.......PTTCCRTTCFHPICCGSSCC 230 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ultra-high-sulfur	ultra-high-sulfur	ultra-high-sulfur	hair keratin cyste	cysteine-rich hair	high sulfur protei	high-sulfur kerati	high-sulfur kerati	keratin high-sulfu	high-sulfur wool m	ultra high-sulfur	keratin high-sulfu	high-sulfur wool m	high-sulfur wool m	hypothetical prote	high-sulfur wool m	keratin high-sulfu	high-sulfur wool m	cysteine-rich prot	high-sulfur wool m	high-sulfur wool m	keratin high-sulfu		keratin KAP5.5 - s	ultra-high-sulfur	hypothetical prote		hypothetical prote	a.
SUMMARIES	ID	A45910	B38346	A38346	S60314	146489	JC6547	S37649	S37650	KRSHHD	147105	S18946	KRSHHA	147106	147107	T30136	147108	KRSHHC	147111	A55035	147109	147112	KRSHHB	146412	I46413	A36686	T29880	KRGT3M	T20561	~
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keratin high-sulfu	Reratin high-sulfu	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
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hynothetial profe	hypothetical prote	hypothetical prote	hypothetical prote	protein R09B5.5 (1	
KRGT3J	KRSHA3	T31561	T16246	D86446	T16840
KRSH3A	JC6548	T31560	B89588	JQ0317	
T23682	T31559	T18593	T23681	A88949	
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284	269.5	263	234.5	232.5	224
279	269	261	234.5	224.5	
274	263	238.5	234.5	224	
32		36 37 38	39 41 41	4 4 4 2 6 4	4.5

ALIGNMENTS

scc 230 1+1 scc 181

228 179

g ò g RESULT 2
B38346
ultra-high-sulfur keratin 2 - mouse
C;Species Mus musculus (house mouse)
C;Date: 31 War-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; B38346
C;Accession: A38660; B38346
C;Accession: A38660; B38346
C;Accession: A38660; Multis, M.; Vogell, G.
C;Accession: A38660; Multis, M.; Vogell, G.
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and ski
A;Reference number: A38660; MULD:91154184; PMID:1840598